

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:20 ; Search time 127.123 Seconds  
(without alignments)  
568.992 Million cell updates/sec

Title: US-10-067-122B-2  
Perfect score: 1428  
Sequence: 1 MGNVCYVIVLLVGCX.....DACSCRCPEEGGGGYEL 256

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1428	100.0	256	2	AAR64199 Murine 4-
2	1428	100.0	256	2	AAR70978 4-1BB rec
3	1428	100.0	256	2	AAW04173 Mouse rec
4	1428	100.0	256	2	AAW26659 Mouse 4-1
5	1428	100.0	256	2	AAY28687 Mouse Rec
6	1428	100.0	256	2	AAY33215 Murine CD
7	1428	100.0	256	5	AAE22581 Mouse rec
8	1428	100.0	256	5	ABB75954 Murine cy
9	1428	100.0	256	7	ADC25939 Murine re
10	1428	100.0	256	7	ADB87549 Mouse rec
11	1085	76.0	191	4	AAB66986 41bb prot
12	795	55.7	255	2	AAR64197 Human 4-1
13	795	55.7	255	2	AAR70977 H4-1BB re
14	795	55.7	255	2	AAW26658 Human 4-1
15	795	55.7	255	2	AAY28688 Human rec
16	795	55.7	255	2	AAY33214 Human CD1
17	795	55.7	255	4	AAE08546 Human h4-
18	795	55.7	255	4	AAE0521 Human tum
19	795	55.7	255	5	ABB75955 Human cyt
20	795	55.7	255	6	ABR39863 Human MOC
21	795	55.7	255	6	ABB84640 Human h4-
22	795	55.7	255	7	AAE39531 Human pro
23	795	55.7	255	7	ADC78803 Human PRO
24	795	55.7	255	7	ADD25599 Binding d
25	795	55.7	255	7	ADE87541 Unknown h

26	782	54.8	255	2	AAW04174	Aaw04174 Human rec
27	768	53.8	255	2	AAR74087	Aar74087 Human rec
28	656	45.9	219	2	AAW31759	Aaw31759 A novel h
29	656	45.9	219	2	AAW92523	Aaw92523 Human h4-
30	656	45.9	219	2	AAW92524	Aaw92524 Human h4-
31	656	45.9	219	4	AAE08545	Aae08545 Human h4-
32	656	45.9	219	6	ABB84639	Abb84639 Human h4-
33	499	34.9	132	3	AAY94714	Aay94714 Tumour ne
34	268	18.8	69	2	AAW94650	Aaw94650 TNF-R ext
35	268	18.8	69	4	AAB69202	Aab69202 Human TNF
36	237	16.6	415	4	AAB36700	Aab36700 Human tum
37	237	16.6	415	6	ABP96138	Abp96138 Mouse lym
38	215	15.1	625	2	AAW83200	Aaw83200 Murine os
39	215	15.1	625	2	AAW69958	Aaw69958 Murine NF
40	215	15.1	625	2	AAW68294	Aaw68294 Murine NF
41	215	15.1	625	2	AAE08739	Aae08739 Murine re
42	215	15.1	625	3	AAE53649	Aay53649 A mouse r
43	215	15.1	625	3	AAE59509	Aay59509 OBM bindi
44	215	15.1	625	4	AAE04427	Aae04427 Murine re
45	215	15.1	625	4	AAE01994	Aae01994 Murine RA

ALIGNMENTS

RESULT 1  
AAR64199  
ID AAR64199 standard; protein; 256 AA.  
XX

AC AAR64199;

XX 25-MAR-2003 (revised)

DT 08-AUG-1995 (first entry)

XX Murine 4-1BB polypeptide.

DE

XX T-cell; lymphocyte; activation; tissue culture; clone; cell lines;

KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.

XX Mus musculus.

XX WO9426290-A1.

PN

XX 24-NOV-1994.

PD

XX 06-MAY-1994; 94WO-US005036.

PF

XX 07-MAY-1993; 93US-00060843.

PR

XX (IMMV ) IMMUNEX CORP.

PA Goodwin RG, Smith CA, Alderson MR;

XX WPI; 1995-022265/03.

DR N-PSDB; AAQ75428.

XX Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB

PT to transduce signal.

XX Example 1; Page 44-45; 65pp; English.

PS The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75422)

XX are useful in a pharmaceutical composition for stimulating the immune

CC system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring

CC mechanisms of T-cell activation, as they are expressed on T lymphocytes.

CC 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation

CC of primary T-cells during the derivation of clonal T-cell lines. It may

CC also be used to stimulate proliferation of activated T-cells, used in

CC therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 256 AA;

SQ Query Match

100.0%; Score 1428; DB 2; Length 256;

Best Local Similarity 100.0%; Pred. No. 1.7e-109;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNVCYNVWVIVLLVGVCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60  
DB 1 MGNVCYNVWVIVLLVGVCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60  
QY 61 CNICRVCAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
DB 61 CNICRVCAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
DB 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLQVLTFLALTSALLLALIFITLLFSLVKWIRKFFPHFKQPFKKTGAAQEEEDACS 240  
DB 181 GHSLQVLTFLALTSALLLALIFITLLFSLVKWIRKFFPHFKQPFKKTGAAQEEEDACS 240  
QY 241 CRCPQEEEGGGGYEL 256  
DB 241 CRCPQEEEGGGGYEL 256

RESULT 2

AAR70978  
ID AAR70978 standard; protein; 256 AA.

XX AC AAR70978;  
DT 25-MAR-2003 (revised)  
DT 16-OCT-1995 (first entry)  
XX 4-1BB receptor protein.  
XX 4-1BB; receptor protein; immunosuppressive; autoimmune disease;  
KW organ transplantation; cell membrane ligand.

OS Mus sp.  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= Sig\_peptide

XX WO9507984-A1.  
XX 23-MAR-1995.  
XX 15-SEP-1994; 94WO-US010457.  
XX 16-SEP-1993; 93US-00122796.  
XX (INDV ) UNIV INDIANA FOUND.

XX Kwon BS;  
XX WPI; 1995-131352/17.  
XX N-PSDB; AAQ86127.  
XX Novel cDNA encoding human receptor protein H4-1BB - useful to produce the  
PT protein which is used to treat autoimmune disease and facilitate organ  
PT transplantation.  
XX Disclosure; Fig 1; 36pp; English.  
XX cDNA encoding the human receptor protein H4-1BB (given in AAQ86126) was  
CC isolated using PCR primers based on the homologous mouse 4-1BB gene  
CC (AAQ86127) encoding mouse receptor protein (AAR70978). (Updated on 25-MAR  
CC -2003 to correct PN field.)  
XX Sequence 256 AA;

Best Local Similarity 100.0%; Pred. No. 1.7e-109;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNVCYNVWVIVLLVGVCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60  
DB 1 MGNVCYNVWVIVLLVGVCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60  
QY 61 CNICRVCAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
DB 61 CNICRVCAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
DB 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLQVLTFLALTSALLLALIFITLLFSLVKWIRKFFPHFKQPFKKTGAAQEEEDACS 240  
DB 181 GHSLQVLTFLALTSALLLALIFITLLFSLVKWIRKFFPHFKQPFKKTGAAQEEEDACS 240  
QY 241 CRCPQEEEGGGGYEL 256  
DB 241 CRCPQEEEGGGGYEL 256

RESULT 3

AAW04173  
ID AAW04173 standard; protein; 256 AA.

XX AC AAW04173;  
DT 12-DEC-1996 (first entry)  
XX Mouse receptor 4-1BB.  
XX Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;  
KW immunostimulant; cancer; autoimmune disease; graft rejection; therapy.

OS Mus sp.  
XX WO9629348-A1.  
XX 26-SEP-1996.  
XX 22-MAR-1996; 96WO-US003965.  
XX 23-MAR-1995; 95US-00409851.  
XX (INDV ) UNIV INDIANA FOUND.  
XX Kwon BS, Kang C;  
XX WPI; 1996-443138/44.  
XX N-PSDB; AAT39541.

XX Monoclonal antibody specific for human receptor protein 4-1BB - used to  
PT enhance proliferation and activation of T-cells for treatment of cancer  
PT and to inhibit specific ligand binding for treating autoimmune diseases.  
XX Disclosure; Page 32-34; 48pp; English.  
XX Novel murine receptor protein 4-1BB (AAW04173) has the potential to  
CC function as an accessory signaling molecule during T-cell activation and  
CC proliferation. It may represent a cell surface molecule involved in T-  
CC cell-APC interactions and may also act as a B-cell costimulator. It is  
CC structurally related to members of the nerve growth factor receptor  
CC superfamily. Its amino acid sequence was deduced from an isolated cDNA  
CC clone (see also AAT39541). A human homologue, H4-1BB (AAW04174), was  
CC identified and used to raise a monoclonal antibody useful in cancer and  
XX autoimmune disease therapy



CC for activation or inhibition of immune response; to block H4-1BB ligand  
 CC binding; treating cancerous tumours and autoimmune diseases; and during  
 CC organ transplantation  
 XX  
 SQ Sequence 256 AA;  
 Query Match 100.0%; Score 1428; DB 2; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-109;  
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGNVCYNVWVIVLLVGVCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60  
 Db 1 MGNVCYNVWVIVLLVGVCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60  
 QY 61 CNICRVCAGYFRFKFCSSTHNAECEEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
 Db 61 CNICRVCAGYFRFKFCSSTHNAECEEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
 QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGPG 180  
 Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGPG 180  
 QY 181 GHSLQVLTFLALTSALLLALIFITLLFSVLKWKIRKPFHFKQPFKKTGAAQEEEDACS 240  
 Db 181 GHSLQVLTFLALTSALLLALIFITLLFSVLKWKIRKPFHFKQPFKKTGAAQEEEDACS 240  
 QY 241 CRCPQEEEGGGGYEL 256  
 Db 241 CRCPQEEEGGGGYEL 256

RESULT 6  
 AAY33215  
 ID AAY33215 standard; protein; 256 AA.  
 XX  
 AC AAY33215;  
 XX  
 DT 18-NOV-1999 (first entry)  
 XX  
 DE Murine CD137 protein.  
 XX  
 KW CD137; monocyte growth factor; proliferation; peripheral monocyte;  
 KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;  
 KW immunostimulatory; non-specific immune response; phagocytosis;  
 KW intracellular destruction; microorganism; immune complex; antibody;  
 KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;  
 KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;  
 KW bacterial; viral infection; immunosuppressant; gene therapy; murine.  
 XX  
 OS Mus sp.  
 XX  
 FN WO9944629-A2.  
 XX  
 PD 10-SEP-1999.  
 XX  
 PF 05-MAR-1999; 99WO-EP001440.  
 XX  
 PR 05-MAR-1998; 98EP-00103859.  
 XX  
 PA (MERC ) MERCKLE GMBH.  
 XX  
 FI Schwarz H, Langstein J;  
 XX  
 DR WPI; 1999-550983/46.  
 XX  
 PT Use of monocyte growth factor CD137 for stimulating proliferation of  
 PT peripheral monocytes, particularly for treating immune deficiency, e.g.  
 PT following cancer therapy.  
 XX  
 PS Disclosure; Fig 1B; 57pp; German.  
 XX  
 CC This invention describes a novel use of the human monocyte growth factor  
 CC CD137, or its functional analogs, for (i) stimulating proliferation of

CC peripheral monocytes; and (ii) treating diseases that are associated with  
 CC disorders of a cellular system that includes monocytes (and/or their  
 CC derived cells, precursor or progenitors) or where the origin and/or  
 CC progression is treatable by stimulating proliferation of such cells. The  
 CC products of the invention have antitumor, antibacterial, antiviral,  
 CC antifungal and immunostimulatory activity. Stimulating proliferation of  
 CC monocytes promotes the non-specific immune response, i.e. it increases  
 CC phagocytosis and intracellular destruction of microorganisms, immune  
 CC complexes and damaged cells, and improves antibody (in)dependent  
 CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat  
 CC diseases associated with a defective immune response where caused by  
 CC inadequate numbers of active monocytes/macrophages, especially damage to  
 CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation  
 CC therapy; disorders of wound healing (e.g. in dialysis or diabetic  
 CC patients, or those with chronic venous insufficiency); tumors; bacterial,  
 CC fungal or viral infections; (non-)congenital or (non-)inherited diseases  
 CC or injury to the immune system; injury induced by treatment with  
 CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune  
 CC disease, or transplant patients). Nucleic acid encoding (I) can be used  
 CC similarly, in gene therapy procedures. Proliferation of peripheral  
 CC monocytes is achieved independently of hematopoietic stem cells. This  
 CC sequence represents the murine CD137 protein described in the method of  
 CC the invention  
 XX  
 SQ Sequence 256 AA;

Query Match 100.0%; Score 1428; DB 2; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-109;  
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGNVCYNVWVIVLLVGVCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60  
 Db 1 MGNVCYNVWVIVLLVGVCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60  
 QY 61 CNICRVCAGYFRFKFCSSTHNAECEEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
 Db 61 CNICRVCAGYFRFKFCSSTHNAECEEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
 QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGPG 180  
 Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGPG 180  
 QY 181 GHSLQVLTFLALTSALLLALIFITLLFSVLKWKIRKPFHFKQPFKKTGAAQEEEDACS 240  
 Db 181 GHSLQVLTFLALTSALLLALIFITLLFSVLKWKIRKPFHFKQPFKKTGAAQEEEDACS 240  
 QY 241 CRCPQEEEGGGGYEL 256  
 Db 241 CRCPQEEEGGGGYEL 256

RESULT 7  
 AAE22581  
 ID AAE22581 standard; protein; 256 AA.  
 XX  
 AC AAE22581;  
 XX  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Mouse receptore 4-1BB protein.  
 XX  
 KW Mouse; lymphokine; L2G25B; macrophage inflammatory protein 1 alpha;  
 KW MIP-1alpha; immune disease; myeloid progenitor cell differentiation;  
 KW 4-1BB; receptor.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT Protein /label= Signal\_peptide  
 FT /note= "Mature receptor 4-1BB protein"  
 FT Modified-site 128..130



XX DT 18-DEC-2003 (first entry)  
XX DE Murine receptor 4-1BB protein.  
XX KW receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;  
XX KW cancer; murine; mouse.  
XX OS Mus musculus.  
XX PN US2003100745-A1.  
XX PD 29-MAY-2003.  
XX PF 04-FEB-2002; 2002US-00067122.  
XX PR 07-NOV-1988; 88US-00267577.  
XX PR 30-JUL-1992; 92US-00922996.  
XX PR 01-FEB-1993; 93US-00012269.  
XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
XX PI Kwon BS;  
XX DR WPI; 2003-678138/64.  
XX DR N-PSDB; ADC25938.  
XX PT New CDNA gene encoding receptor protein 4-1BB, useful for isolating  
PT similar DNA sequences, and the encoded polypeptide and an antibody to it,  
PT useful for identifying ligands, and for modulating immune cell activity.  
XX PS Claim 7; Fig 2; 77pp; English.  
XX CC The invention relates to a novel CDNA gene encoding receptor protein 4-  
CC 1BB. The CDNA gene of the invention demonstrates immunostimulant  
CC activities and may be useful as a probe to isolate DNA sequences encoding  
CC for proteins similar to the receptor protein encoded by the DNA. The  
CC protein, its fragments and derivatives may be useful as a probe to  
CC isolate ligands to receptor protein 4-1BB, for stimulating proliferation  
CC of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand  
CC binding. The antibody may be useful for enhancing T-cell proliferation or  
CC activation. Finally, the invention may be useful with respect to cancer  
CC research. The current sequence is that of the murine receptor 4-1BB  
CC protein of the invention.  
XX SQ Sequence 256 AA;  
Query Match 100.0%; Score 1428; DB 7; Length 256;  
Best Local Similarity 100.0%; Pred. No. 1.7e-109;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNNCYNVVIVILLVGCCKVAVQNSCDNCQPGTFCKYKYNPVCKSCPSTFSSIGGQPN 60  
Db 1 MGNNCYNVVIVILLVGCCKVAVQNSCDNCQPGTFCKYKYNPVCKSCPSTFSSIGGQPN 60  
QY 61 CNICRVACGYFRFKFCSSTHNAECIEGFGHCLGPQCTRCCKDCRPGQELTKQCKTCS 120  
Db 61 CNICRVACGYFRFKFCSSTHNAECIEGFGHCLGPQCTRCCKDCRPGQELTKQCKTCS 120  
QY 121 LGTFNDQNGTGVCPRWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCPRWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLOVTLFLALTSALLLALIFITLLFSVLKWKIRKFPFHIFKQPFKTTGAQBEDACS 240  
Db 181 GHSLOVTLFLALTSALLLALIFITLLFSVLKWKIRKFPFHIFKQPFKTTGAQBEDACS 240  
QY 241 CRCPQEEGGGGYEL 256  
Db 241 CRCPQEEGGGGYEL 256

ADE87549  
ID ADE87549 standard; protein; 256 AA.  
XX AC ADE87549;  
XX DT 29-JAN-2004 (first entry)  
XX DE Mouse receptor H4-1BB.  
XX KW immunosuppressive; H4-1BB ligand binding blocker; mouse;  
KW receptor protein; H4-1BB; B-cell proliferation stimulator;  
KW T-cell proliferation enhancer; immune system supressor; transplantation;  
KW autoimmune disease.  
XX OS Mus sp.  
XX PN US2003082157-A1.  
XX PD 01-MAY-2003.  
XX PF 12-JUN-2002; 2002US-00170997.  
XX PR 07-NOV-1988; 88US-00267577.  
XX PR 30-JUL-1992; 92US-00922996.  
XX PR 01-FEB-1993; 93US-00012269.  
XX PR 05-JUN-1995; 95US-00460976.  
XX PR 22-OCT-1997; 97US-00955573.  
XX PA (KWON/) KWON B S.  
XX PI Kwon BS;  
XX DR WPI; 2003-576599/54.  
XX DR N-PSDB; ADE87548.  
XX PT New CDNA, or its encoded receptor protein H4-1BB, useful as probes to  
PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking  
PT H4-1BB ligand binding to facilitate organ transplantation or treat  
PT autoimmune diseases.  
XX PS Disclosure; Fig 1; 19pp; English.  
XX CC The invention describes a CDNA, which encodes for human receptor protein  
CC H4-1BB. The CDNA, or its fragments or derivatives, are useful as a probe  
CC to isolate DNA sequences encoding for proteins similar to the receptor  
CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or  
CC derivatives, is useful as a probe for identifying ligands to the receptor  
CC protein H4-1BB, or for stimulating the proliferation of B-cells  
CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are  
CC useful for enhancing T-cell proliferation of activation. The CDNA or  
CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand  
CC binding, which is particularly useful for suppressing the immune system  
CC during transplantation, or for treating autoimmune diseases. This is the  
CC amino acid sequence of mouse receptor H4-1BB.  
XX SQ Sequence 256 AA;  
Query Match 100.0%; Score 1428; DB 7; Length 256;  
Best Local Similarity 100.0%; Pred. No. 1.7e-109;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNNCYNVVIVILLVGCCKVAVQNSCDNCQPGTFCKYKYNPVCKSCPSTFSSIGGQPN 60  
Db 1 MGNNCYNVVIVILLVGCCKVAVQNSCDNCQPGTFCKYKYNPVCKSCPSTFSSIGGQPN 60  
QY 61 CNICRVACGYFRFKFCSSTHNAECIEGFGHCLGPQCTRCCKDCRPGQELTKQCKTCS 120  
Db 61 CNICRVACGYFRFKFCSSTHNAECIEGFGHCLGPQCTRCCKDCRPGQELTKQCKTCS 120  
QY 121 LGTFNDQNGTGVCPRWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCPRWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180

QY	181	GHSLOVLTFLALTSALLALIFITLLFSLVKWIRKKPPHIFKQPFKKTGTAQEEDACS	240
Db	181	GHSLOVLTFLALTSALLALIFITLLFSLVKWIRKKPPHIFKQPFKKTGTAQEEDACS	240
QY	241	CRCPOEEGGGGGYEL	256
Db	241	CRCPOEEGGGGGYEL	256
RESULT 11			
AAB66986	AAB66986 standard; protein; 191 AA.		
XX	AC	AAB66986;	
XX	DT	19-APR-2001 (first entry)	
XX	DE	41bb protein.	
XX	KW	Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;	
XX	KW	multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;	
XX	KW	systemic lupus erythematosus; graft-versus-host disease; septic shock;	
XX	KW	acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;	
XX	KW	coronary condition; myocardial infarction; cancer; diabetes; psoriasis;	
XX	KW	endometriosis; fever; glomerulonephritis; inflammatory bowel disease;	
XX	KW	ischaemia; Parkinson's disease.	
XX	OS	Unidentified.	
XX	PN	WO200103719-A2.	
XX	PD	18-JAN-2001.	
XX	PF	07-JUL-2000; 2000WO-US018667.	
XX	PR	09-JUL-1999; 99US-00350670.	
XX	PR	09-DEC-1999; 99US-00457647.	
XX	PA	(AMGE-) AMGEN INC.	
XX	PI	Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;	
XX	DR	WPI; 2001-103031/11.	
XX	PT	Treating conditions leading to bone loss such as rheumatoid arthritis,	
XX	PT	multiple sclerosis and asthma, comprises administering an osteoprotegerin	
XX	PT	protein in conjunction with e.g. inhibitors of interleukin and tumor	
XX	PT	necrosis factor alpha.	
XX	PS	Disclosure; Fig 2; 316pp; English.	
XX	CC	The present invention relates to a method for treating conditions leading	
XX	CC	to bone loss. The method comprises administering a purified and isolated	
XX	CC	osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)	
XX	CC	in conjunction with other substances such as tumour necrosis factor-alpha	
XX	CC	(TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE	
XX	CC	modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet	
XX	CC	activating factor (PAF) antagonists. The method is useful for treating	
XX	CC	conditions leading to bone loss such as rheumatoid arthritis, multiple	
XX	CC	sclerosis, osteoporosis, osteomyelitis and asthma. The method is also	
XX	CC	useful for treating inflammation, systemic lupus erythematosus (SLE) and	
XX	CC	graft-versus-host disease (GVHD). Other diseases that can be treated	
XX	CC	include acute pancreatitis, Alzheimer's disease, anorexia,	
XX	CC	atherosclerosis, coronary conditions (e.g. myocardial infarction),	
XX	CC	cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,	
XX	CC	inflammatory bowel disease, ischaemia, pain, Parkinson's disease,	
XX	CC	psoriasis and septic shock. The present sequence was used in a sequence	
XX	CC	homology comparison	
XX	SQ	Sequence 191 AA;	
QY	Query Match 76.0%; Score 1085; DB 4; Length 191;		
Db	Best Local Similarity 100.0%; Pred. No. 2.1e-81;		

Matches	191;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	MGNNCYNVVVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCCKSCPPSTFSSIGGQPN	60						
Db	1	MGNNCYNVVVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCCKSCPPSTFSSIGGQPN	60						
QY	61	CNLCRVACAGYFRFKFCSSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKQGCKTCS	120						
Db	61	CNLCRVACAGYFRFKFCSSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKQGCKTCS	120						
QY	121	LGTENDQNGTGVCPRWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGPG	180						
Db	121	LGTENDQNGTGVCPRWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGPG	180						
QY	181	GHSLOVLTFL 191							
Db	181	GHSLOVLTFL 191							
RESULT 12									
AAR64197	AAR64197 standard; protein; 255 AA.								
XX	AC	AAR64197;							
XX	DT	25-MAR-2003 (revised)							
XX	DT	08-AUG-1995 (first entry)							
XX	DE	Human 4-1BB polypeptide.							
XX	KW	T-cell; lymphocyte; activation; tissue culture; clone; cell lines;							
XX	KW	proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.							
XX	OS	Homo sapiens.							
XX	PN	WO9426290-A1.							
XX	PD	24-NOV-1994.							
XX	PF	06-MAY-1994; 94WO-US005036.							
XX	PR	07-MAY-1993; 93US-00060843.							
XX	PA	(IMMV ) IMMUNEX CORP.							
XX	PI	Goodwin RG, Smith CA, Alderson MR;							
XX	DR	WPI; 1995-022265/03.							
XX	DR	N-PSDB; AAQ75424.							
XX	PT	Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB							
XX	PT	to transduce signal.							
XX	PS	Claim 39; Page 47-48; 65pp; English.							
XX	CC	The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75423)							
XX	CC	are useful in a pharmaceutical composition for stimulating the immune							
XX	CC	system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring							
XX	CC	mechanisms of T-cell activation, as they are expressed on T lymphocytes.							
XX	CC	4-1BB-L can be used as a tissue culture reagent for in vitro cultivation							
XX	CC	of primary T-cells during the derivation of clonal T-cell lines. It may							
XX	CC	also be used to stimulate proliferation of activated T-cells, used in							
XX	CC	therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)							
XX	SQ	Sequence 255 AA;							
Query Match 55.7%; Score 795; DB 2; Length 255;									
Best Local Similarity 58.4%; Pred. No. 2.1e-57;									
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;									
QY	1	MGNNCYNVVVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCCKSCPPSTFSSIGGQPN	59						
Db	1	MGNNSYNIVATLLVLNFERTRSLQDPCSNCPAGTFCDDNNRNQICSPCPPNFSFSGAGQR	60						

QY 60 NCNIRVCAGYFRFKKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGCSMCEQDCKQGQELTKKGCKDC 120  
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPPHIFKQPFKKTGAQAE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPOEEEG 250  
Db 238 EDGSCRFPEEEEG 252

RESULT 13  
AAR70977  
ID AAR70977 standard; protein; 255 AA.  
XX  
AC AAR70977;  
XX  
DT 25-MAR-2003 (revised)  
DT 16-OCT-1995 (first entry)  
XX  
DE H4-1BB receptor protein.  
XX  
KW H4-1BB; receptor protein; immunosuppressive; autoimmune disease;  
KW organ transplantation; cell membrane ligand.  
XX  
OS Homo sapiens.  
XX  
PN WO9507984-A1.  
XX  
PD 23-MAR-1995.  
XX  
PF 15-SEP-1994; 94WO-US010457.  
XX  
PR 16-SEP-1993; 93US-00122796.  
XX  
PA (INDV ) UNIV INDIANA FOUND.  
XX  
PI Kwon BS;  
XX  
DR WPI; 1995-131352/17.  
DR N-PSDB; AAQ86126.  
XX

Novel cDNA encoding human receptor protein H4-1BB - useful to produce the protein which is used to treat autoimmune disease and facilitate organ transplantation.  
Claim 6; Fig 2; 36pp; English.  
Human peripheral blood lymphocyte-derived cDNA was amplified by PCR using probes based on the mouse receptor protein 4-1BB gene. The PCR product was used to screen a cDNA library of activated human T-cells. The isolated cDNA (AAQ86126), deposited as NRRL AAB21131, encoded the human homolog, H4-1BB (AAR70977), of 4-1BB. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 2; Length 255;  
Best Local Similarity 58.4%; Pred. No. 2.1e-57;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
QY 1 MGNVCNVVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNVCNVIVATLLLVLFNFTSRSLQDPCSNCPAGTFCDNRRNQCSPCPPNFSAGGQR 60  
QY 60 NCNIRVCAGYFRFKKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTC 119

Db 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGCSMCEQDCKQGQELTKKGCKDC 120  
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPPHIFKQPFKKTGAQAE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPOEEEG 250  
Db 238 EDGSCRFPEEEEG 252

RESULT 14  
AAW26658  
ID AAW26658 standard; protein; 255 AA.  
XX  
AC AAW26658;  
XX  
DT 25-MAR-2003 (revised)  
DT 25-FEB-1998 (first entry)  
XX  
DE Human 4-1BB receptor.  
XX  
KW 4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte; T cell;  
KW proliferation; immunostimulant.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .23  
FT /label= Sig\_peptide  
FT Domain 24. .186  
FT /label= Cytoplasmic  
FT Modified-site 115. .117  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 126. .128  
FT /note= "Asn is N-glycosylated"  
FT Domain 187. .213  
FT /label= Transmembrane  
FT Domain 214. .255  
FT /label= Extracellular  
XX  
PN US5674704-A.  
XX  
PD 07-OCT-1997.  
XX  
PF 06-MAY-1994; 94US-00236918.  
XX  
PR 07-MAY-1993; 93US-00060843.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Alderson MR, Goodwin RG, Smith CA;  
XX  
DR WPI; 1997-502333/46.  
DR N-PSDB; AAT91026.  
XX  
PT DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell proliferation in vitro, and as research tools.  
XX  
PS Example 2; Col 43-44; 32pp; English.  
XX  
CC This protein comprises human 4-1BB, a member of the tumour necrosis factor receptor superfamily that is expressed on cells that include, but are not limited to, stimulated human peripheral blood lymphocytes. Its amino acid sequence was deduced from an isolated cDNA clone (see AAT91026) obtained from human peripheral blood T-lymphocytes. A novel claimed cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned and sequenced (see AAW26657) that binds to 4-1BB. 4-1BB-L,



XX Use of monocyte growth factor CD137 for stimulating proliferation of  
PT peripheral monocytes, particularly for treating immune deficiency, e.g.  
PT following cancer therapy.  
XX  
PS Claim 12; Fig 1A; 57pp; German.  
XX  
CC This invention describes a novel use of the human monocyte growth factor  
CC CD137, or its functional analogs, for (i) stimulating proliferation of  
CC peripheral monocytes; and (ii) treating diseases that are associated with  
CC disorders of a cellular system that includes monocytes (and/or their  
CC derived cells, precursor or progenitors) or where the origin and/or  
CC progression is treatable by stimulating proliferation of such cells. The  
CC products of the invention have antitumor, antibacterial, antiviral,  
CC antifungal and immunostimulatory activity. Stimulating proliferation of  
CC monocytes promotes the non-specific immune response, i.e. it increases  
CC phagocytosis and intracellular destruction of microorganisms, immune  
CC complexes and damaged cells, and improves antibody (in)dependent  
CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat  
CC diseases associated with a defective immune response where caused by  
CC inadequate numbers of active monocytes/macrophages, especially damage to  
CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation  
CC therapy; disorders of wound healing (e.g. in dialysis or diabetic  
CC patients; or those with chronic venous insufficiency); tumors; bacterial,  
CC fungal or viral infections; (non-)congenital or (non-)inherited diseases  
CC or injury to the immune system; injury induced by treatment with  
CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune  
CC disease, or transplant patients). Nucleic acid encoding (I) can be used  
CC similarly, in gene therapy procedures. Proliferation of peripheral  
CC monocytes is achieved independently of hematopoietic stem cells. This  
CC sequence represents the human CD137 protein described in the method of  
CC the invention  
XX  
SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 2; Length 255;  
Best Local Similarity 58.4%; Pred. No. 2.1e-57;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
QY 1 MGNVCYVNVVIVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNVCYVNVVIVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPPSTFSSIGGQP 60  
QY 60 NCNCRVCAGYFRFKFCSSTHNAECIEGFGHCLGPGQTRCEKDCRPGQELTKGCKTC 119  
Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFHCGLGAGCSMCEQDCKQGLTKGCKDC 120  
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGRSVLVNGTKERDVVCGPPVVSFSPSTTISVTPEGGP 177  
QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFHFKQPFKKTGAAQE 235  
Db 178 AREPGHSQVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFHFKQPFKKTGAAQE 237  
QY 236 EDACSCRCPEEGG 250  
Db 238 EDGCSRCRPEEGG 252

RESULT 17  
AAE08546  
ID AAE08546 standard; protein; 255 AA.  
XX AAE08546;  
AC AAE08546;  
XX 15-NOV-2001 (first entry)  
XX Human h4-1BB receptor.  
XX Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;  
XX tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxin shock;  
KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;  
KW

KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;  
KW bone resorption; human immunodeficiency virus; HIV; graft rejection;  
KW inflammation; antibacterial; immunosuppressive; vulnary; vasotropic;  
KW antiinflammatory; protozoicide; cachexia; immunomodulator; virucide.  
XX  
OS Homo sapiens.  
XX  
PN US2001014465-A1.  
XX  
PD 16-AUG-2001.  
XX  
PF 19-DEC-2000; 2000US-00739394.  
XX  
PR 15-MAR-1996; 96US-0013474P.  
PR 13-MAR-1997; 97US-00816605.  
PR 22-FEB-1999; 99US-00253549.  
XX  
PA (NIJJ/) NI J.  
PA (YUGG/) YU G.  
PA (GENT/) GENTZ R.  
PA (DILL/) DILLON P J.  
XX  
PI Ni J, Yu G, Gentz R, Dillon PJ;  
XX WPI; 2001-529104/58.  
XX  
PT New human 4-1BB receptor splicing variant polypeptides and  
PT polynucleotides, useful for research, diagnosis, prevention and treatment  
PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency  
PT syndrome and graft rejection.  
XX  
PS Disclosure; Fig 2; 28pp; English.  
XX  
CC The present invention relates to an isolated human 4-1BB receptor  
CC splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis  
CC factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in  
CC gene therapy. h4-1BBSV is useful for research, biological, clinical and  
CC therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives  
CC are useful as an immunogen to produce antibodies which are useful for  
CC isolating and identifying clones expressing the polypeptide or to purify  
CC the polypeptide. h4-1BBSV is useful for diagnosis and treatment of  
CC disorders of cells, tissues and organisms and its nucleic acid is useful  
CC for detecting complementary polynucleotides for e.g. as a diagnostic  
CC reagent and for chromosomal identification. h4-1BBSV receptor agonists  
CC are useful for preventing, treating tumours, restenosis, cytotoxicity,  
CC bacterial and viral infection, deleterious effects of ionising radiation,  
CC autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-  
CC host rejection, to regulate immune responses, wound healing and cellular  
CC proliferation and antagonists are useful for treating and/or preventing  
CC endotoxin shock, inflammation, cerebral malaria, activation of human  
CC immunodeficiency virus (HIV) virus, bone resorption, graft rejection and  
CC cachexia. The present sequence is human h4-1BB receptor  
XX  
SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 4; Length 255;  
Best Local Similarity 58.4%; Pred. No. 2.1e-57;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
QY 1 MGNVCYVNVVIVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNVCYVNVVIVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPPSTFSSIGGQP 60  
QY 60 NCNCRVCAGYFRFKFCSSTHNAECIEGFGHCLGPGQTRCEKDCRPGQELTKGCKTC 119  
Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFHCGLGAGCSMCEQDCKQGLTKGCKDC 120  
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGRSVLVNGTKERDVVCGPPVVSFSPSTTISVTPEGGP 177  
QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFHFKQPFKKTGAAQE 235  
Db 178 AREPGHSQVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFHFKQPFKKTGAAQE 237  
QY 236 EDACSCRCPEEGG 250  
Db 238 EDGCSRCRPEEGG 252

Db 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVGRKKLLYIFKQPFMRPVQTTQE 237

QY 236 EDACSCRCPOEEEGG 250

Db 238 EDGSCRFPEEEEGG 252

RESULT 18

AAB50521

ID AAB50521 standard; protein; 255 AA.

XX AC AAB50521;

XX XX 15-MAR-2001 (first entry)

DT XX Human tumour necrosis factor receptor 4-1BB protein SEQ ID NO:11.

DE XX Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; neutropic;

XX KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;

KW KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;

KW KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;

KW KW anticonvulsant; antiparasitic; cardiant; anti-HIV; tumourkinsonian;

KW KW gene therapy; restenosis; graft versus host disease; tumour; cancer;

KW KW apoptotic cell death related disease; autoimmune disorder;

KW KW cardiovascular disorder; viral infection.

XX XX Homo sapiens.

OS XX WO200071150-A1.

PN XX 30-NOV-2000.

PD XX 18-MAY-2000; 2000WO-US013515.

PF XX 20-MAY-1999; 99US-0135164P.

PR XX (HUMA-) HUMAN GENOME SCI INC.

XX XX Wei Y, Ruben SM, Gentz RL, Ni J;

PI WPI; 2001-041051/05.

XX DR Nucleic acid encoding a TRID polypeptide, also referred to as tumor

XX PT necrosis factor receptor 5, useful in the diagnosis, treatment or

PT PT prevention of cancer, autoimmune disorders and viral infection.

PT XX Disclosure; Fig 2; 285pp; English.

PS XX The present invention describes the human TRID protein (tumour necrosis

XX CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without

CC CC intracellular domain, also referred to as tumour necrosis factor receptor

CC CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, neutropic,

CC CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,

CC CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic

CC CC activities, and can be used in gene therapy. The TRID polynucleotides are

CC CC useful for detecting complementary polynucleotides. TRID proteins and

CC CC polynucleotides are useful in the treatment of tumours, resistance to

CC CC parasite, bacteria and viruses, restenosis and graft versus host disease.

CC CC They are also useful for inducing proliferation of T-cells, endothelial

CC CC cells and certain haematopoietic cells, to regulate antiviral responses

CC CC and to prevent certain autoimmune diseases after stimulation of TRID by

CC CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID

CC CC polypeptides are useful for treating and/or preventing diseases

CC CC associated with increased or decreased apoptotic cell death. The TRID

CC CC polynucleotides, proteins, antibodies, agonists and antagonists are

CC CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)

CC CC autoimmune disorders; (c) diseases associated with increased apoptosis;

CC CC (d) cardiovascular disorders; and (e) viral infection. The present

CC CC sequence represents a tumour necrosis factor receptor used in comparison

CC CC with TRID in the exemplification of the present invention

XX XX Sequence 255 AA;

SQ

Query Match 55.7%; Score 795; DB 4; Length 255;

Best Local Similarity 58.4%; Pred. No. 2.1e-57;

Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCVNVVIVLLLVGCEKVGAVQNSCDNCQPGTFC-RKYNFVCKSCPPSTFSSIGGQP 59

Db 1 MGNSCVNIVATLLLVLPNFRTRSLQDPCSNCPAGTFCDDNNRNIQICSPCPNSFSSAGGQR 60

QY 60 NCNICVCAGYFRFKFCSTHNAECIEGFHCLGPQCTRCCKDCRFGQELTKQGCKTC 119

Db 61 TCDICRQCKGVFTRKECSSTNAECDCTPGFHCLGAGCSMCEQDCKQOELTKKGCKDC 120

QY 120 SLGTFNDQGTGVCPRWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGP 179

Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177

QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSLVKWIRKKFPHIFKQPFKKTGAQAE 235

Db 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVGRKKLLYIFKQPFMRPVQTTQE 237

QY 236 EDACSCRCPOEEEGG 250

Db 238 EDGSCRFPEEEEGG 252

RESULT 19

ABB75955

ID ABB75955 standard; protein; 255 AA.

XX AC ABB75955;

XX XX 12-JUL-2002 (first entry)

DT XX Human cytokine receptor 4-1BB.

DE XX Cytokine; receptor; 4-1BB; human.

XX KW Homo sapiens.

XX OS

XX FH Key

FT Peptide

FT Protein

FT Domain

FT Modified-site

FT Modified-site

FT Region

FT Domain

FT US6355779-B1.

XX 12-MAR-2002.

XX 10-SEP-1998; 98US-00150864.

XX 07-MAY-1993; 93US-00060843.

PR 06-MAY-1994; 94US-00236918.

PR 05-AUG-1997; 97US-00910449.

XX (IMMV ) IMMUNEX CORP.

PI Goodwin RG; Smith CA, Alderson MR;

XX WPI; 2002-380940/41.

DR N-PSDB; ABL54048.

XX New antibody specific for the cytokine 4-1BB-ligand, useful for

PT

PT immunoaffinity purification of the ligand.  
XX Example 2; Col 43-44; 31pp; English.  
PS  
XX  
XX  
CC The present sequence is the protein sequence of the human cytokine  
CC receptor, 4-1BB. The sequence was deduced from a cDNA clone (see  
CC AB54048) obtained from a human peripheral blood T-lymphocyte cDNA  
CC library. It shows 60% identity to murine 4-1BB (see AB575954). A portion  
CC of the extracellular (ligand binding) domain of the human 4-1BB cytokine  
CC receptor was utilised in a human 4-1BB/human IGF1 Fc fusion protein,  
CC which was used to identify the human 4-1BB ligand (4-1BB-L, see  
CC AB575953). The invention provides novel murine and human 4-1BB-L  
CC polypeptides and human 4-1BB polypeptides, as well as DNA sequences  
CC encoding them, recombinant expression vectors and host cells, and methods  
CC for producing the novel polypeptides by cultivating the transformed host  
CC cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from  
CC their extracellular domains, have therapeutic value. Antibodies that are  
CC immunoreactive with 4-1BB-L or human 4-1BB are claimed  
XX  
SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 5; Length 255;  
Best Local Similarity 58.4%; Pred. No. 2.1e-57;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
QY 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPSTFSSIGGQP 59  
Db 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPSTFSSIGGQP 60  
QY 60 NCNVCAGYFRFKFCSSSTHNAECIEGFCGLGQCTCEKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGCSNCEQDCKQGLTKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNKTGKRDVVCSPADLSPGAS-SVTTP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFPHFKQPFKTTGAQAE 235  
Db 178 AREPGHSPQIISFFLALTSTALLFLFLTLRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPOEEEGG 250  
Db 238 EDGCSRCRFPPEEEGG 252

RESULT 20  
ABR39863  
ID ABR39863 standard; protein; 255 AA.  
XX  
AC ABR39863;  
XX  
DT 11-AUG-2003 (first entry)  
DE Human MOCEPTIN polypeptide.  
XX  
KW MOCEPTIN; tumour necrosis factor receptor; TNF receptor; anorectic;  
KW antilipemic; antiarteriosclerotic; antidiabetic; cerebroprotective;  
KW hypotensive; immunomodulator; antidepressant; human; receptor.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Peptide  
FT Location/Qualifiers  
FT 1..17  
FT /note= "putative signal peptide"  
FT 18..255  
FT /note= "mature protein"  
FT 18..186  
FT /note= "extracellular domain"  
FT 187..213  
FT /note= "transmembrane domain"  
FT 214..255

XX PN WO2003011325-A1.  
XX  
XX  
PD 13-FEB-2003.  
XX  
PF 25-JUL-2002; 2002WO-IB003499.  
XX  
PR 27-JUL-2001; 2001US-0308142P.  
XX  
PA (GEST ) GENSET SA.  
XX  
XX Lucas J, Dialynas D, Briggs K;  
PI  
XX WPI; 2003-268084/26.  
DR N-PSDB; ACC47324.  
DR  
XX  
PT New agonist and antagonist of MOCEPTIN (a member of the Tumor Necrosis  
PT Factor Receptor family) activity, useful for preventing or treating  
PT obesity-related diseases (e.g. hyperlipidemia or stroke), or increasing  
PT body mass.  
XX  
PS Disclosure; Page 32-33; 37pp; English.  
XX  
XX The invention relates to an agonist or antagonist of MOCEPTIN (a member  
CC of the Tumour Necrosis Factor Receptor family) activity. The antagonist  
CC or agonist of MOCEPTIN activity, or the composition comprising the  
CC agonist or antagonist, is useful for preventing or treating an obesity-  
CC related disorder or disease in an individual. In particular, the agonist  
CC of MOCEPTIN activity is useful for treating or preventing obesity-related  
CC diseases, e.g. hyperlipidemia, atherosclerosis, insulin resistance,  
CC diabetes, stroke or hypertension. The agonist is also useful for reducing  
CC body mass and maintaining weight loss. The antagonist of MOCEPTIN  
CC activity is useful for increasing body mass, or for treating or  
CC preventing disorders associated with excessive weight loss, e.g.  
CC cachexia, cancer-related weight loss, AIDS-related weight loss, chronic  
CC inflammatory disease-related weight loss, or anorexia. The present  
CC sequence represents a human MOCEPTIN polypeptide  
XX  
SQ Sequence 255 AA;

Query Match 55.7%; Score 795; DB 6; Length 255;  
Best Local Similarity 58.4%; Pred. No. 2.1e-57;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
QY 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPSTFSSIGGQP 59  
Db 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCPGTFRC-RKYNPVCKSCPSTFSSIGGQP 60  
QY 60 NCNVCAGYFRFKFCSSSTHNAECIEGFCGLGQCTCEKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTNAECDCTPGFHLGAGCSNCEQDCKQGLTKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNKTGKRDVVCSPADLSPGAS-SVTTP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFPHFKQPFKTTGAQAE 235  
Db 178 AREPGHSPQIISFFLALTSTALLFLFLTLRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPOEEEGG 250  
Db 238 EDGCSRCRFPPEEEGG 252

RESULT 21  
ABR84640  
ID ABR84640 standard; protein; 255 AA.  
XX  
AC ABR84640;  
XX  
DT 05-FEB-2003 (first entry)

DE Human h4-1BB receptor.

KW Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive; anti-HIV; antibacterial; anti-inflammatory; protozoacide; immunomodulator; vasotropic; gene therapy; chromosome mapping; extracellular domain; endotoxic shock; cytotoxicity; cerebral malaria; autoimmune disease; human immunodeficiency virus; HIV; graft-host rejection; bone resorption; cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome; AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis; autoimmune disease; h4-1BB.

XX Homo sapiens.

OS US2002127651-A1.

PN 12-SEP-2002.

XX 15-MAR-2002; 2002US-00097330.

PR 15-MAR-1996; 96US-0013474P.

PR 13-MAR-1997; 97US-00815505.

PR 22-FEB-1999; 99US-00253549.

PR 19-DEC-2000; 2000US-00739394.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Gentz RL, Dillon PJ;

PI WPI; 2003-066900/06.

XX Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors, providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells, and to treat restenosis.

PT Disclosure; Fig 2; 29pp; English.

XX This invention describes a novel human h4-1BBSV receptor or a sequence that is at least 85% identical to the h4-1BBSV receptor. The product of the invention has anti-tumour, virucide, immunosuppressive, anti-HIV, antibacterial, anti-inflammatory, protozoacide, immunomodulator and vasotropic activity and can be used for gene therapy and chromosome mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to a disease related to underexpression of h4-1BBSV or for identifying agonists and antagonists. The soluble extracellular domain of h4-1BBSV receptor polypeptide is useful for treating and/or preventing endotoxic shock, cytotoxicity, inflammation, cerebral malaria, activation of human immunodeficiency virus (HIV), graft-host rejection, bone resorption or cachexia, tumours, autoimmune disease, ionizing radiation, acquired immunodeficiency syndrome (AIDS), for providing resistance to bacteria, viruses and parasites, to induce proliferation of endothelial cells and certain haematopoietic cells, to treat restenosis and to prevent certain autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist. This sequence represents the human 4-1BB receptor described in the disclosure of the invention

XX Sequence 255 AA;

Query Match 55.7%; Score 795; DB 6; Length 255;  
Best Local Similarity 58.4%; Pred. No. 2.1e-57;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNVCYNIVATLLVLNFRTRSLQDPCSNCPAGTFCDDNRRNQICSPCPNPSFSSAGGQR 60

QY 60 NCNICRVAGYFRFKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHLGAGCSMCEQDCKQGLTKGCKDC 120

QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVVCGPPWVSFSPSTTISVTPEGGP 179  
Db 121 CFGTENDQK-RGICRPTWNTNCSLDGKSVLVNKGTKERDVVCGSPADLSPGAS-SVTTP-AP 177

QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFKPHIFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLFLLTRFVSVKRGRKLLLYIFKQPFMRPVQTQE 237

QY 236 EDACSCRCPOEEEGG 250  
Db 238 EDGSCRFPEEEEGG 252

RESULT 22  
AAE39531  
ID AAE39531 standard; protein; 255 AA.  
XX  
AC AAE39531;  
DT 18-DEC-2003 (first entry)  
XX  
DE Human protein SEQ ID NO: 2.  
XX  
KW Human; adhesive; packaging.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 107  
FT /note= "Encoded by AGA"

XX US2003000851-A1.  
XX  
PD 02-JAN-2003.  
XX  
PF 08-JUN-2001; 2001US-00877336.  
XX  
PR 08-JUN-2001; 2001US-00877336.

XX (WALS/) WALSH J C.  
PA (HAWK/) HAWKINS K E.  
XX Walsh JC, Hawkins KE;  
PI  
XX WPI; 2003-266968/26.  
DR N-PSDB; AAD59981.

XX Paper board container manufacture for soap boxes, involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to another direction.

PS Disclosure; Page 12-13; 46pp; English.

XX The invention relates to a method and apparatus for applying adhesive to packaging in a variety of configurations. The method involves applying adhesive on blank while moving in one direction, which is folded, and then another quantity of adhesive is applied before moving blank to another direction. The invention is useful for e.g. soap boxes, cereal boxes, bottle carriers, can boxes. The present sequence is human protein. Note: There is no specific information about the sequence in the specification

XX Sequence 255 AA;

Query Match 55.7%; Score 795; DB 7; Length 255;  
Best Local Similarity 58.4%; Pred. No. 2.1e-57;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCPGTF-C-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNVCYNIVATLLVLNFRTRSLQDPCSNCPAGTFCDDNRRNQICSPCPNPSFSSAGGQR 60

QY 60 NCNICRVAGYFRFKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHLGAGCSMCEQDCKQGLTKGCKDC 120

QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTPP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKPPHIFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPEEEGG 250  
Db 238 EDGSCRFPEEEGG 252  
RESULT 23  
ADC78803  
ID ADC78803 standard; protein; 255 AA.  
AC ADC78803;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Human PRO protein #16.  
XX  
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;  
KW Crohn's disease.  
XX  
OS Homo sapiens.  
XX  
PN WO2003034984-A2.  
XX  
PD 01-MAY-2003.  
XX  
PF 15-OCT-2002; 2002WO-US033070.  
XX  
PR 19-OCT-2001; 2001US-0340083P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Goddard A, Gurney AL;  
XX  
DR WPI; 2003-481990/45.  
DR N-PSDB; ADC78802.  
XX  
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a  
PT medicament for diagnosing or treating cancer or inflammatory bowel  
PT disorder e.g., ulcerative colitis or Crohn's disease.  
XX  
PS Claim 12; SEQ ID NO 32; 327pp; English.  
XX  
CC The invention comprises the amino acid and coding sequences of human PRO  
CC proteins. The DNA and protein sequences of the invention are useful for  
CC the diagnosis and treatment of cancer and inflammatory bowel disease  
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid  
CC sequence represents a human PRO protein of the invention.  
XX  
SQ Sequence 255 AA;  
Query Match 55.7%; Score 795; DB 7; Length 255;  
Best Local Similarity 58.4%; Pred. No. 2.1e-57;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
QY 1 MGNNCYNVVIVILLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNSCYNIVATLLLVLFNFRTRSLQDPCSNCPAGTFCDDNRRNQICSPCPNFSFSSAGGQR 60  
QY 60 NCNICRVAGYFRFKFCSSSTHNAECIEGFHCLGPOCTRCEKDCRPGQELTKGCKTC 119  
Db 61 TCDICRQCKGVFTRKESSTNAECDTPGFHCLGAGCSMCEQDCKQGQELTKGCKDC 120  
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTPP-AP 177

QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKPPHIFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPEEEGG 250  
Db 238 EDGSCRFPEEEGG 252  
RESULT 24  
ADD25599  
ID ADD25599 standard; protein; 255 AA.  
XX  
AC ADD25599;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Binding domain-immunoglobulin fusion protein-associated protein #77.  
XX  
KW Binding domain; immunoglobulin; fusion protein; cytostatic;  
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
KW neuroprotective; hinge region; immunoglobulin heavy chain;  
KW CH2 constant region; CH3 constant region; IgG1;  
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
XX  
OS Unidentified.  
XX  
PN US2003118592-A1.  
XX  
PD 26-JUN-2003.  
XX  
PF 25-JUL-2002; 2002US-00207655.  
XX  
PR 17-JAN-2001; 2001US-0367358P.  
PR 17-JAN-2002; 2002US-00053530.  
PR 03-JUN-2002; 2002US-0385691P.  
XX  
PA (GENE-) GENE-CRAFT INC.  
XX  
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
XX  
DR WPI; 2003-801317/75.  
XX  
PT New binding domain-immunoglobulin fusion protein, useful for treating a  
PT subject having or suspected of having a malignant condition or a B-cell  
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
XX  
SQ Disclosure; SEQ ID NO 160; 157pp; English.  
CC The invention relates to a binding domain-immunoglobulin fusion protein  
CC comprising a binding domain polypeptide that is fused to an  
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
CC CH2 constant region polypeptide that is fused to the hinge region  
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
CC polypeptide that is fused to the CH2 constant region polypeptide. The  
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin  
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
CC region polypeptide, derived from (a) having 3 or more cysteine residues;  
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
CC immunoglobulin hinge region polypeptide contains no more than one  
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
CC capable of at least one immunological activity comprising antibody  
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
CC binding domain polypeptide is capable of specifically binding to an



PN WO9629348-A1.  
 XX 26-SEP-1996.  
 PD 22-MAR-1996; 96WO-US003965.  
 XX 23-MAR-1995; 95US-00409851.  
 XX (INDV ) UNIV INDIANA FOUND.  
 XX Kwon BS, Kang C;  
 PI WPI; 1996-443138/44.  
 DR N-PSDB; AAT39546.  
 XX Monoclonal antibody specific for human receptor protein 4-1BB - used to enhance proliferation and activation of T-cells for treatment of cancer and to inhibit specific ligand binding for treating autoimmune diseases.  
 PT Disclosure; Page 36-37; 48pp; English.  
 XX Novel human receptor protein H4-1BB (AAW04174) has the potential to function as an accessory signaling molecule during T-cell activation and proliferation. Its amino acid sequence was deduced from a cDNA clone (AAT39546) isolated from activated human T-lymphocytes. Recombinant H4-1BB can be produced in transfected host cells. It is used to isolate receptor ligands, to stimulate B-cells expressing such ligands and to block H4-1BB ligand binding. A fusion protein of H4-1BB with human placental alkaline phosphatase can be used to modify immune responses. A monoclonal antibody raised against an immunopeptide (see also AAW04172) of H4-1BB is useful in the treatment of cancer and autoimmune diseases  
 XX Sequence 255 AA;  
 SQ

Query Match 54.8%; Score 782; DB 2; Length 255;  
 Best Local Similarity 58.0%; Pred. No. 2.5e-56;  
 Matches 148; Conservative 31; Mismatches 68; Indels 8; Gaps 6;

QY 1 MGNVCYNVIVVILLVGGCKVAVQNSDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGP 59  
 Db 1 MGNVCYNIVATLLVLFNFRTRSLQDPCSNCPAGTFCDDNNRNQICSPPPNSFSSAGQR 60  
 QY 60 NCNCRVCAGYFRFKFCSSSTHNAECIEGHCGLGQCTRCCKDRCRPGQELTKQCKTC 119  
 Db 61 TCDICRQCKGVFRTRKESSTNSAECDCPTGPHCLGAGCSMCEQDCKQGLTKKCKDC 120  
 QY 120 SLGTFNDQNGTGVCRPWTCNSLDGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
 Db 121 CFGTFNDQK-RGICRPCTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177  
 QY 180 G---GHSQVLTFLALTS-ALLALIFITLLFSLVKWIRKKFPHFKQPFKKTGAQAE 235  
 Db 178 AREPGHSPQIISFFLALTSTALLFLFLTLRFSVVKGRKLLYIFKQPFMRPVQTTQE 237  
 QY 236 EDACSCRCPEEEGG 250  
 Db 238 EDGCSRCFPEEEGG 252

RESULT 27  
 AAR74087  
 ID AAR74087 standard; protein; 255 AA.  
 XX  
 AC AAR74087;  
 XX  
 DT 21-JAN-1996 (first entry)  
 XX  
 DE Human receptor induced by lymphocyte activation (ILA).  
 XX  
 KW ILA; receptor inducible by lymphocyte activation; disease diagnosis;  
 KW antiinflammatory.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..17  
 FT /note= "signal peptide"  
 FT Misc-difference 138  
 FT /note= "potential N-glycosylation site"  
 FT Misc-difference 149  
 FT /note= "potential N-glycosylation site"  
 FT Domain 187..213  
 FT /note= "transmembrane domain"  
 FT Misc-difference 234  
 FT /note= "casein-kinase-II phosphorylation site"  
 FT Misc-difference 235  
 FT /note= "casein-kinase-II phosphorylation site"  
 FT Binding-site 241..244  
 FT /note= "potential ligand binding site"  
 FT Misc-difference 242  
 FT /note= "protein-kinase phosphorylation site"  
 XX  
 PN CA2108401-A.  
 XX  
 PD 28-MAR-1995.  
 XX  
 PF 14-OCT-1993; 93CA-02108401.  
 XX  
 PR 27-SEP-1993; 93US-00127693.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Lotz M, Schwarz H;  
 XX WPI; 1995-194420/26.  
 DR N-PSDB; AAR74087.  
 XX  
 PT New receptor inducible by lymphocyte activation - used to develop prods.  
 PT for the diagnosis and treatment of inflammatory host defence pathology.  
 XX  
 PS Claim 55; Page 61; 91pp; English.  
 XX  
 CC ILA may be used to identify a host defence inflammatory response in body tissue. The ILA agents can be used to detect an ILA-mediated pathology such as atherosclerosis, autoimmune disease (rheumatoid arthritis, transplanted rejection, pathogenic host defense responses to microorganism and malignancy such as lung carcinoma  
 XX  
 SQ Sequence 255 AA;

Query Match 53.8%; Score 768; DB 2; Length 255;  
 Best Local Similarity 57.6%; Pred. No. 3.5e-55;  
 Matches 147; Conservative 30; Mismatches 70; Indels 8; Gaps 6;  
 QY 1 MGNVCYNVIVVILLVGGCKVAVQNSDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGP 59  
 Db 1 MGNVCYNIVATLLVLFNFRTRSLQDPCSNCPAGTFCDDNNRNQICSPPPNSFSSAGQR 60  
 QY 60 NCNCRVCAGYFRFKFCSSSTHNAECIEGHCGLGQCTRCCKDRCRPGQELTKQCKTC 119  
 Db 61 TCDIWRQCKGVFRTRKESSTNSAECDCPTGPHCLGAGCSMCEQDCKQGLTKKCKDC 120  
 QY 120 SLGTFNDQNGTGVCRPWTCNSLDGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
 Db 121 CFGTFNDQK-RGICRPCTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177  
 QY 180 G---GHSQVLTFLALTS-ALLALIFITLLFSLVKWIRKKFPHFKQPFKKTGAQAE 235  
 Db 178 AREPGHSPQIISFFLALTSTALLFLFLTLRFSVVKGRKLLYIFKQPFMRPVQTTQE 237  
 QY 236 EDACSCRCPEEEGG 250  
 Db 238 EDGCSRCFPEEEGG 252

AAW31759  
ID AAW31759 standard; protein; 219 AA.  
XX  
AC AAW31759;  
XX  
DT 01-APR-1998 (first entry)  
XX  
DE A novel human h4-1BBSV receptor.  
XX  
KW h4-1BBSV receptor; 4-1BB receptor splicing variant; endotoxigenic shock;  
KW tumour necrosis factor; TNF ligand; T-cell activation; inflammation;  
KW tumour prevention; viral infection; autoimmune disease;  
KW cellular proliferation.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..18  
FT /note= "putative signal sequence"  
FT Protein 19..219  
FT /note= "mature protein"  
FT Domain 19..150  
FT /note= "soluble extracellular domain"  
FT Domain 151..177  
FT /note= "transmembrane domain"  
XX  
PN WO9733898-A1.  
XX  
PD 18-SEP-1997.  
XX  
PF 15-MAR-1996; 96WO-US003587.  
XX  
PR 15-MAR-1996; 96WO-US003587.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ni J, Yu G, Gentz RL;  
XX  
DR WPI; 1997-470806/43.  
DR N-PSDB; AAT88969.  
XX  
PT Human 4-1BB receptor splicing variant and related DNA - used to develop  
PT products for treating e.g. tumours, viral infection, endotoxigenic shock,  
PT autoimmune disease or bone resorption.  
XX  
PS Claim 15; Fig 1; 73pp; English.  
XX  
CC The present sequence represents a novel human h4-1BBSV receptor. This is  
CC a human 4-1BB receptor splicing variant. The 4-1BB ligand is a member of  
CC the tumour necrosis factor (TNF) family of ligands. It is induced by T-  
CC cell activation. The h4-1BBSV receptor nucleic acid and protein can be  
CC used for diagnosis and therapy. In particular, agonists of h4-1BBSV  
CC receptor can be used to treat and/or prevent tumours, restenosis,  
CC cytotoxicity, bacterial and viral infection, deleterious effects of  
CC ionising radiation, autoimmune disease, AIDS and graft-host rejection, to  
CC regulate immune responses, wound healing and cellular proliferation.  
CC Antagonists can be used to treat and/or prevent endotoxigenic shock,  
CC inflammation, cerebral malaria, activation of the HIV virus, graft  
CC rejection, bone resorption and cachexia  
XX  
SQ Sequence 219 AA;  
Query Match 45.9%; Score 656; DB 2; Length 219;  
Best Local Similarity 51.2%; Pred. No. 4.9e-46;  
Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;  
QY 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCQPGTFCRKNVPVCKSCPSTFSSIGGQPN 60  
DB 1 MGNVCYNIVATLLVLFNFRTRSLQDPCSNCP-----  
QY 61 CNICRVACGYFRFKFCSTHNAECIEGFGHCLGPQCTRCCKDCRPGQELTKQGKTC 120  
DB 33 -----AGVFRTRKESSTNAECCTPGFHLGAGCMCEQDCRQGLTKGCKDCC 85

121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
86 FGTFNDQK-RGICRPWTNCSLDGRSVLVNGTKERDVVCGPSSADLSPGAS-SVTTP-APA 142  
181 ---GHSIQVLTFLALTS-ALLLALIFITLLFSLVKWIRKKFPHFKQPFKTTGAAQEE 236  
143 REPCHSPQIIISFFLALTSTALLFLFLTLRFSVYKGRKLLYIFKQPFMRPVQTTQEE 202  
237 DACSCRCPEEEGG 250  
203 DGCSCRFPEEEGG 216  
RESULT 29  
AAW92523  
ID AAW92523 standard; protein; 219 AA.  
XX  
AC AAW92523;  
XX  
DT 23-APR-1999 (first entry)  
XX  
DE Human h4-1BBSV receptor protein.  
XX  
KW h4-1BBSV receptor; human; splice variant; antagonist; treatment;  
KW disease prevention; endotoxigenic shock; inflammation; cerebral malaria;  
KW HIV virus activation; graft rejection; bone resorption; cachexia;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..18  
FT /label= signal\_peptide  
FT Protein 19..219  
XX  
PN US5874240-A.  
XX  
PD 23-FEB-1999.  
XX  
PF 13-MAR-1997; 97US-00816605.  
XX  
PR 15-MAR-1996; 96US-0013474P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Dillon PJ, Yu G, Ni J, Gentz R;  
XX  
DR WPI; 1999-179974/15.  
DR N-PSDB; AAX02162.  
XX  
PT New nucleic acid encoding human 4-1BB receptor splicing variant - useful  
PT in treating h4-1BBSV mediated disease states such as endotoxigenic shock,  
PT inflammation, graft rejection and inactivation of HIV.  
XX  
PS Claim 1a; Fig 1A-B; 28pp; English.  
XX  
CC This sequence represents a novel human h4-1BBSV receptor protein which is  
CC used in a method for making a human 4-1BB receptor splice variant which  
CC acts as an antagonist. The antagonist polypeptides may be used to  
CC treat/prevent disease states mediated by h4-1BBSV receptors such as  
CC endotoxigenic shock, inflammation, cerebral malaria, activation of the HIV  
CC virus, graft rejection, bone resorption and cachexia. The h4-1BBSV coding  
CC sequences are useful in gene therapy  
XX  
SQ Sequence 219 AA;  
Query Match 45.9%; Score 656; DB 2; Length 219;  
Best Local Similarity 51.2%; Pred. No. 4.9e-46;  
Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;  
QY 1 MGNVCYNVIVLLVGCCKVAVQNSCDNCQPGTFCRKNVPVCKSCPSTFSSIGGQPN 60

Db 1 MGNVCYNIVATLLVLFNFRTRSLQDPCSNCP----- 32

QY 61 CNICRVACGYFRFKKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120

Db 33 -----AGVFRTRKECSSTSNACEDCTPGFHLGAGCSMCEQDCKQGLTKKGCKDCC 85

QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGPG 180

Db 86 FGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTPP-APA 142

QY 181 ---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPPHIFKQPFKTTGAAQEE 236

Db 143 REPCHSPQIIISFFLALTSTALLFLFLTLFSLVVRGRKKLLYIFKQPFMRPVQTTQEE 202

QY 237 DACSCRCPQEEGG 250

Db 203 DGCSCRFPEEEGG 216

RESULT 30

AAW92524

ID AAW92524 standard; protein; 219 AA.

XX AAW92524;

XX 23-APR-1999 (first entry)

XX Human h4-1BBSV receptor protein variant.

DE h4-1BBSV receptor; human; splice variant; antagonist; treatment;

KW disease prevention; endotoxin shock; inflammation; cerebral malaria;

KW HIV virus activation; graft rejection; bone resorption; cachexia;

KW gene therapy.

XX Homo sapiens.

OS Synthetic.

XX Key

XX Location/Qualifiers

FT Misc-difference 33..34

FT /note= "Site of deletion of residues GTFCDNRRNQICSPC

FT PNPSSAGGQRTCDICROCK corresponding to amino acid

FT residues 34-69 of the wild-type protein"

XX US5874240-A.

XX 23-FEB-1999.

PF 13-MAR-1997; 97US-00816605.

XX 15-MAR-1996; 96US-0013474P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Dillon PJ, Yu G, Ni J, Gentz R;

XX WPI; 1999-179974/15.

XX New nucleic acid encoding human 4-1BB receptor splicing variant - useful

PT in treating h4-1BBSV mediated disease states such as endotoxin shock,

PT inflammation, graft rejection and inactivation of HIV.

XX Claim 29; Page; 28pp; English.

XX This sequence represents a human h4-1BBSV receptor protein variant which

CC has antagonistic properties. This protein may be used to treat/prevent

CC disease states mediated by h4-1BBSV receptors such as endotoxin shock,

CC inflammation, cerebral malaria, activation of the HIV virus, graft

CC rejection, bone resorption and cachexia. The h4-1BBSV coding sequences

CC are useful in gene therapy. This sequence does not appear in the

CC specification but has been created from the wild-type sequence

XX represented in Fig 2

XX Sequence 219 AA;

SQ

Query Match 45.9%; Score 656; DB 2; Length 219;

Best Local Similarity 51.2%; Pred. No. 4.9e-46;

Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;

QY 1 MGNVCYNIVVIVLLVGVCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPSTSSIGGQPN 60

Db 1 MGNVCYNIVATLLVLFNFRTRSLQDPCSNCP----- 32

QY 61 CNICRVACGYFRFKKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120

Db 33 -----AGVFRTRKECSSTSNACEDCTPGFHLGAGCSMCEQDCKQGLTKKGCKDCC 85

QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGPG 180

Db 86 FGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTPP-APA 142

QY 181 ---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPPHIFKQPFKTTGAAQEE 236

Db 143 REPCHSPQIIISFFLALTSTALLFLFLTLFSLVVRGRKKLLYIFKQPFMRPVQTTQEE 202

QY 237 DACSCRCPQEEGG 250

Db 203 DGCSCRFPEEEGG 216

RESULT 31

AAE08545

ID AAE08545 standard; protein; 219 AA.

XX AAE08545;

XX 15-NOV-2001 (first entry)

XX Human h4-1BB splicing variant (h4-1BBSV) receptor.

DE Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;

KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxin shock;

KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;

KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;

KW bone resorption; human immunodeficiency virus; HIV; graft rejection;

KW inflammation; antibacterial; immunosuppressive; vulnery; vasotropic;

KW antiinflammatory; protozoicide; cachexia; immunomodulator; virucide.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

FT Peptide 1..18

FT /label= Signal\_peptide

FT Protein 19..219

FT /label= Mature\_human\_h4-1BBSV\_receptor

FT Domain 19..150

FT /label= Extracellular\_domain

FT Domain 151..177

FT /label= Transmembrane\_domain

XX US2001014465-A1.

XX 16-AUG-2001.

XX 19-DEC-2000; 2000US-00739394.

XX 15-MAR-1996; 96US-0013474P.

PR 13-MAR-1997; 97US-00816605.

PR 22-FEB-1999; 99US-00253549.

XX (NIJ/) NI J.

PA (YUGG/) YU G.

PA (GENT/) GENTZ R.

PA (DILL/) DILLON P J.

XX Ni J, Yu G, Gentz R, Dillon PJ;

XX



QY 121 LGTFNDQNGTGVCPWNTNCSLDGRSVLKTGTEKDVWCGPPVVSFSPSTTISVTPEGGPG 180  
DQ 86 FGTFNDQK-RGICSPWNTNCSLDGRSVLNGTKERDVWCGPSADLSPGAS-SVTTP-APA 142  
QY 181 ---GHSQVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPHIFKQPFKKTGAQEE 236  
DQ 143 REPGHSPQIISFFLALTSTALLFLFFLTFRFSVVVGRKKLLYIFKQPFVRPVQTTQEE 202  
QY 237 DACSCRPQEEGG 250  
DQ 203 DGCSCRFPEEEGG 216

RESULT 33  
AA94714  
ID AA94714 standard; protein; 132 AA.  
XX  
AC AA94714;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Tumour necrosis factor receptor (TNFR) domain of 4-1BB protein.  
XX  
KW Tumour necrosis factor-receptor related protein; TR2; human; cancer;  
KW Chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;  
KW immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;  
KW severely combined immunodeficiency; apoptosis inhibition;  
KW Alzheimer's disease; Parkinson's disease; Crohn's disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200056405-A2.  
XX  
PD 28-SEP-2000.  
XX

PF 22-MAR-2000; 2000WO-US007521.  
XX  
PR 22-MAR-1999; 99US-0125683P.  
PR 26-MAR-1999; 99US-0126522P.  
PR 20-MAY-1999; 99US-0135169P.  
PR 06-AUG-1999; 99US-0147383P.  
XX

PA (NIJJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (GENTZ/) GENTZ R L.  
XX

PI Ni J, Rosen CA, Gentz RL;  
XX  
WPI; 2000-594519/56.  
XX

PT Nucleic acid molecule encoding a human tumor necrosis factor receptor 2  
PT and its two splice variants, useful for treating arthritis or  
PT inflammation, cancer (such as follicular lymphomas) and immunodeficiency  
PT disorders.  
XX

PS Disclosure; Fig 16; 373pp; English.  
XX

CC This invention relates to an isolated nucleic acid molecule encoding a  
CC human tumour necrosis factor (TNF)-receptor related protein TR2. Included  
CC in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.  
CC The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a  
CC member of the TNFR superfamily. The invention includes a method for the  
CC treatment of arthritis or inflammation using an antibody directed against  
CC a fragment of the TR2 protein. TR2 its agonists, antagonists and  
CC antibodies exhibit cytostatic, dermatological, antianemic,  
CC immunosuppressive, antiallergic, antiarthritic, antiparkinsonian, and  
CC antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and  
CC cerebroprotective activity. The methods are useful for treating arthritis  
CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53  
CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an  
CC immunodeficiency or for enhancing an in vivo leukocyte response to an  
CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or

CC preventing autoimmune diseases (such as autoimmune haemolytic anaemia,  
CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and  
CC inflammatory myopathies) and immunodeficiency disorders (such as severely  
CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative  
CC disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,  
CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or  
CC antagonists are useful for treating or preventing autoimmune diseases and  
CC inhibit the growth, progression and/or metastasis of cancers. They are  
CC also used to activate, differentiate or proliferate cancerous cells or  
CC tissues, and can be used to treat diseases associated with increased cell  
CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,  
CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful  
CC as sources for generating antibodies, as molecular weight markers. This  
CC sequence represents the tumour necrosis factor receptor (TNFR) domain of  
CC the human 4-1BB protein. The sequence was used in the characterisation of  
CC the TR2 receptor protein of the invention  
XX  
SQ Sequence 132 AA;

Query Match 34.9%; Score 499; DB 3; Length 132;  
Best Local Similarity 63.9%; Pred. No. 2.3e-33;  
Matches 85; Conservative 13; Mismatches 33; Indels 2; Gaps 2;  
QY 28 CDNCQPGTFC-RKYNPVCKSQPSTFSSIGQPNICRVAGYFRFKFCSSTHNAECE 86  
Db 1 CSNCPAGTFCNRRNQICSPQPPNSFSSAGGQRTCDICRQCKGVFTRKESSTSAECD 60  
QY 87 CIEGFHCLGPQCTCEKDCRPGQELTKQCKTCSLGTENDQNGTGVCRPWNTNCSLDGRSV 146  
Db 61 CTPGFHCLGAGCSMCEQDCKQQLTKKCKDCCFCGTFNKQK-RGICRPWNTNCSLDGKSV 119  
QY 147 LKGTGTEKDVVCG 159  
Db 120 LVNGTKERDVVCG 132

RESULT 34  
AAW94650  
ID AAW94650 standard; peptide; 69 AA.  
XX  
AC AAW94650;  
XX  
DT 29-APR-1999 (first entry)  
XX  
DE TNF-R extracellular Cys-rich domain 4-1BB.  
XX

KW Tumour necrosis factor receptor; TNF-R; autoimmune diseases;  
KW inflammation; septic shock; cachexia; graft versus host disease;  
KW skin allergic reaction; immune complex disease; malaria;  
KW transplantation rejection.  
XX

OS Homo sapiens.  
XX

PN WO9853842-A1.  
XX

PD 03-DEC-1998.  
XX

PF 29-MAY-1998; 98WO-US010891.  
XX

PR 30-MAY-1997; 97US-00866545.  
XX

PA (UYPE-) UNIV PENNSYLVANIA.  
XX

PI Greene MI, Murali R, Takasaki W;  
XX

DR WPI; 1999-080781/07.  
XX

PT New compounds designed from a binding loop of a tumour necrosis factor  
PT receptor - are capable of inhibiting the biological activities of tumour  
PT necrosis factor, e.g., in treating inflammation or autoimmune diseases.  
XX  
PS Disclosure; Fig 1; 78pp; English.  
XX

CC The present invention describes peptides and peptide analogues which  
CC correspond in primary sequence to a binding loop of a tumour necrosis  
CC factor receptor (TNF-R) superfamily member. The compounds are especially  
CC designed from a binding loop of TNF-R p55. They are capable of inhibiting  
CC TNF binding to its cellular receptors and may be used to inhibit the  
CC biological activities of TNF. They may be used in treating TNF-associated  
CC conditions such as acute and chronic inflammatory responses, septic  
CC shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic  
CC reactions, immune complex disease, transplantation rejection and malaria.  
CC Administration is, e.g. oral, transdermal, transmucosal, pulmonary,  
CC subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5  
CC mg/kg/day. The present sequence represents an extracellular Cys-rich  
CC domain of TNF-R from the present invention

XX  
SQ Sequence 69 AA;

Query Match 18.8%; Score 268; DB 2; Length 69;  
Best Local Similarity 63.8%; Pred. No. 1.2e-14;  
Matches 44; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 44 CKSCPPSTFSSIGGQPNICRVCAGYFRFKKFCSSSTHNAECIEGFHCLGPQCTRCEK 103  
DB 1 CSPCPNPSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECDCTPGFHLGAGCSMCEQ 60

QY 104 DCRPGQELT 112  
DB 61 DCKQGQELT 69

RESULT 35  
AAB69202  
ID AAB69202 standard; protein; 69 AA.

AC AAB69202;

DT 30-APR-2001 (first entry)

DE Human TNF-R extracellular Cys-rich domain 4-IBB SEQ ID NO:11.

XX Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;  
KW osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic;  
KW antirheumatic; antiarthritic; antiinflammatory; immunomodulatory;  
KW tumour necrosis factor-related activation-induced cytokine; TRANCE;  
KW receptor activator of NF-kappaB ligand; RANK; osteoporosis;  
KW Paget's disease; metastatic bone disease; rheumatoid arthritis;  
KW periodontal disease; modulating dendritic cell maturation;  
KW T cell proliferation; CD40 receptor system.

XX Homo sapiens.

XX WO200108699-A1.

PD 08-FEB-2001.

XX 28-JUL-2000; 2000WO-US020510.

XX 28-JUL-1999; 99US-0146090P.

XX (UYPE-) UNIV PENNSYLVANIA.

PA (AOKI/) AOKI K.

PA (HORN/) HORNE W C.

PA (BARO/) BARON R.

XX Aoki K, Horne WC, Baron R, Greene MI, Murali R;

XX WPI; 2001-182866/18.

PT Use of peptides and peptide analogs which are TRANCE/RANK inhibitors, for  
PT inhibiting osteoclastogenesis and bone resorption.

XX Disclosure; Fig 1; 81pp; English.

CC The present invention describes a method for inhibiting

CC osteoclastogenesis and bone resorption. Osteoclastogenesis and bone  
CC resorption inhibiting peptide analogues from the present invention have  
CC osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory  
CC and immunomodulatory activities, and are tumour necrosis factor (TNF)-  
CC related activation-induced cytokine (TRANCE)/receptor activator of NF-  
CC kappaB ligand (RANK) inhibitors. The method is useful for treating  
CC diseases characterised by bone loss such as osteoporosis, Paget's  
CC disease, metastatic bone disease, rheumatoid arthritis or periodontal  
CC disease, and modulating dendritic cell maturation, T cell proliferation,  
CC and/or CD40 receptor systems. The present sequence represents an  
CC extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-  
CC R) superfamily member, which is used in the exemplification of the  
CC present invention

XX  
SQ Sequence 69 AA;

Query Match 18.8%; Score 268; DB 4; Length 69;  
Best Local Similarity 63.8%; Pred. No. 1.2e-14;  
Matches 44; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 44 CKSCPPSTFSSIGGQPNICRVCAGYFRFKKFCSSSTHNAECIEGFHCLGPQCTRCEK 103  
DB 1 CSPCPNPSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECDCTPGFHLGAGCSMCEQ 60

QY 104 DCRPGQELT 112  
DB 61 DCKQGQELT 69

RESULT 36  
AAB36700  
ID AAB36700 standard; protein; 415 AA.

AC AAB36700;

DT 15-MAR-2001 (first entry)

DE Human tumour necrosis factor receptor LTbR protein SEQ ID NO:6.

XX Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;  
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;  
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;  
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;  
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;  
KW apoptotic cell death related disease; autoimmune disorder;  
KW cardiovascular disorder; viral infection.

XX Homo sapiens.

XX WO200071150-A1.

PD 30-NOV-2000.

XX 18-MAY-2000; 2000WO-US013515.

XX 20-MAY-1999; 99US-0135164P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Wei Y, Ruben SM, Gentz RL, Ni J;

XX WPI; 2001-041051/05.

XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
XX necrosis factor receptor 5, useful in the diagnosis, treatment or  
XX prevention of cancer, autoimmune disorders and viral infection.

XX Disclosure; Fig 2; 285pp; English.

XX The present invention describes the human TRID protein (tumour necrosis  
XX factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
XX intracellular domain, also referred to as tumour necrosis factor receptor

CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nootropic,  
CC neuroprotective, antiviral, anti-inflammatory, anticonvulsant,  
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic  
CC activities, and can be used in gene therapy. The TRID polynucleotides are  
CC useful for detecting complementary polynucleotides. TRID proteins and  
CC polynucleotides are useful in the treatment of tumours, resistance to  
CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
CC They are also useful for inducing proliferation of T-cells, endothelial  
CC cells and certain haematopoietic cells, to regulate antiviral responses  
CC and to prevent certain autoimmune diseases after stimulation of TRID by  
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
CC polypeptides are useful for treating and/or preventing diseases  
CC associated with increased or decreased apoptotic cell death. The TRID  
CC polynucleotides, proteins, antibodies, agonists and antagonists are  
CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)  
CC autoimmune disorders; (c) diseases associated with increased apoptosis;  
CC (d) cardiovascular disorders; and (e) viral infection. The present  
CC sequence represents a tumour necrosis factor receptor used in comparison  
CC with TRID in the exemplification of the present invention

XX SQ Sequence 415 AA;

Query Match 16.6%; Score 237; DB 4; Length 415;  
Best Local Similarity 27.0%; Pred. No. 3e-11;  
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCQPGTF-----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVACGYFRFKKF--CSS 79  
Db 59 CSRCPGGEFVFAVCSRSQDTVCKTCPHNSYNEHNLSTCQLCRPCDIVLGFEVAPCTS 118  
QY 80 THNAECECIEGFHC--LGPQCTRCEKD-----CRPGQEL-----TKGCKTCSLGF- 124  
Db 119 DRKAECRCQPGMSCVYLDNECVHCEERLVLCQPGTEAEVTDEIMDTVNCVCPKPGHFQ 178  
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVVSFSPSTTISVTPEGGPGGHS 184  
Db 179 NTSSPRARCOQPHTRCEIQGLVEAAGPAGTSYSDTICKNP-----PEPG----- 219  
QY 185 QVLTFLALTSALLLALIFITLLFSLVKWIR-----KKEPHIFKQPFKKTGAQAEEDAC 239  
Db 220 --AMLLAILLSLVLFLLFTTVL--ACAWMRHPSLCRKLGLTLLKR-----HPEGES 268  
QY 240 SCRCPOEE 247  
Db 269 PCPAPRAD 276

RESULT 37  
ABP96138  
ID ABP96138 standard; protein; 415 AA.

XX AC ABP96138;  
XX AC  
XX AC  
DT 09-MAY-2003 (first entry)  
XX DE Mouse lymphotoxin-beta receptor protein SEQ ID NO:20.  
XX KW Human; tumour necrosis factor receptor 2 related protein variant;  
KW TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;  
KW TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;  
KW asthma; ulcerative colitis.

XX OS Mus musculus.  
XX PN WO2003012037-A2.  
XX PD 13-FEB-2003.  
XX PF 24-JUL-2002; 2002WO-US023684.  
XX PR 27-JUL-2001; 2001US-00917372.  
XX PA (INCY-) INCYTE GENOMICS INC.

XX

Lal PG, Warren BA;  
WPI; 2003-256445/25.

XX New CDNA, useful for preparing a composition for treating a disease or  
PT condition associated with increased TNF signaling e.g., cancer of the  
PT prostate, ovary, gallbladder, breast, brain, liver or colon, or  
PT rheumatoid arthritis, asthma.

XX Disclosure; Fig 2A-C; 64pp; English.

XX The present invention describes human tumour necrosis factor receptor 2  
CC related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic  
CC and immunosuppressive activities, and can be used in gene therapy. The  
CC TNFR2PV cDNA or protein sequences can be used for preparing a composition  
CC for treating a disease or condition associated with increased TNF  
CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,  
CC brain, liver or colon, or inflammatory disorders, such as rheumatoid  
CC arthritis, asthma or ulcerative colitis. The present sequence represents  
CC a mouse lymphotoxin-beta receptor amino acid sequence, which is given in  
CC comparison with human TNFR2PV in the exemplification of the present  
CC invention

XX SQ Sequence 415 AA;

Query Match 16.6%; Score 237; DB 6; Length 415;  
Best Local Similarity 27.0%; Pred. No. 3e-11;  
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCQPGTF-----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVACGYFRFKKF--CSS 79  
Db 59 CSRCPGGEFVFAVCSRSQDTVCKTCPHNSYNEHNLSTCQLCRPCDIVLGFEVAPCTS 118  
QY 80 THNAECECIEGFHC--LGPQCTRCEKD-----CRPGQEL-----TKGCKTCSLGF- 124  
Db 119 DRKAECRCQPGMSCVYLDNECVHCEERLVLCQPGTEAEVTDEIMDTVNCVCPKPGHFQ 178  
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVVSFSPSTTISVTPEGGPGGHS 184  
Db 179 NTSSPRARCOQPHTRCEIQGLVEAAGPAGTSYSDTICKNP-----PEPG----- 219  
QY 185 QVLTFLALTSALLLALIFITLLFSLVKWIR-----KKEPHIFKQPFKKTGAQAEEDAC 239  
Db 220 --AMLLAILLSLVLFLLFTTVL--ACAWMRHPSLCRKLGLTLLKR-----HPEGES 268  
QY 240 SCRCPOEE 247  
Db 269 PCPAPRAD 276

RESULT 38  
AAW83200  
ID AAW83200 standard; protein; 625 AA.

XX AC AAW83200;  
XX AC  
DT 11-FEB-1999 (first entry)  
XX DE Murine osteoclast differentiation and activation receptor.  
XX KW Osteoprotegerin binding protein; OPG binding protein; arthritis;  
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;  
KW hypercalcaemia; osteoclast differentiation and activation receptor;  
KW Paget's disease.

XX OS Mus sp.  
XX PN WO9846751-A1.  
XX PD 22-OCT-1998.  
XX PF 15-APR-1998; 98WO-US007584.

XX 16-APR-1997; 97US-00842842.  
PR 23-JUN-1997; 97US-0080855.  
PR 30-MAR-1998; 98US-00052521.  
XX (AMGE-) AMGEN INC.  
XX Boyle WJ;  
PI WPI; 1998-594578/50.  
DR N-PSDB; AAV70304.  
XX  
PT Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g.  
PT treating bone diseases by modulating osteoclast differentiation and for  
PT diagnosis.  
XX  
PS Example 12; Fig 10; 47pp; English.  
XX  
CC The present sequence represents murine osteoclast differentiation and  
CC activation receptor (ODAR). The present invention describes  
CC osteoprotegerin (OPG) binding protein. Host cells transfected with  
CC vectors containing nucleic acid molecules encoding OPG binding protein  
CC are used to produce recombinant OPG binding protein. OPG binding protein  
CC is used in binding assays to determine osteoprotegrin (OG) in biological  
CC samples; to screen for specific binding agents (particularly agonists and  
CC antagonists, including intracellular proteins); to raise Ab (useful in  
CC immunoassays for detection of OPG binding protein) and to identify  
CC compounds that modulate binding of OPG binding protein to ODAR. The  
CC nucleic acid molecule encoding OPG binding protein can be used to detect  
CC OPG binding protein-encoding sequences, e.g. screening for related  
CC sequences, also to produce transgenic animal models, while complementary  
CC sequences are used for antisense regulation of OPG binding protein  
CC expression. Modulators of OPG binding protein, particularly soluble forms  
CC of OPG binding protein or Ab, are used to treat or prevent bone diseases,  
CC e.g. osteoporosis, bone loss caused by arthritis or metastases,  
CC hypercalcaemia, Paget's disease, periodontal disease, osteoporosis,  
CC loosening of prostheses, optionally in combination with agents that  
CC promote bone growth  
XX  
SQ Sequence 625 AA;  
Query Match 15.1%; Score 215; DB 2; Length 625;  
Best Local Similarity 28.6%; Pred. No. 3e-09;  
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;  
QY 28 CDNCQPGTF-CRKNP-----VCKSCPSTF-SSIGQPNICRVACGYFRFKFCSSTH 81  
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKLLHKVCDAGKALVAVDPGNH 107  
QY 82 NA--ECECIEGFH-----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127  
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVF 164  
QY 128 NGTGVCPRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSIQV 186  
Db 165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSMTLRRPKEAQAYLPSLIV 217  
QY 187 LTLFLALTSALLLALIF-----ITLLFVLKWKIRKFFPHIFKQPFKKTGAQAQBEDA 238  
Db 218 LLLFISV--VVAAIIFGVYRKGGKALTANLWNWV-----NDA 254  
QY 239 CSCRCQEEEGG 250  
Db 255 CSSLSGNKESG 266  
RESULT 39  
AAW69958  
ID AAW69958 standard; protein; 625 AA.  
XX  
AC AAW69958;  
XX  
DT 08-OCT-1998 (first entry)

XX Murine NF-kB receptor activator muRANK.  
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;  
KW immune response; inflammatory response; toxic shock; sepsis; RANKL;  
KW RANK ligand; tumour necrosis factor; TNF; murine.  
XX  
OS Mus sp.  
XX WO9828426-A2.  
XX 02-JUL-1998.  
XX 22-DEC-1997; 97WO-US023775.  
XX 23-DEC-1996; 96US-0059978P.  
PR 07-MAR-1997; 97US-00813509.  
PR 14-OCT-1997; 97US-0064671P.  
XX (IMMV ) IMMUNEX CORP.  
PA Anderson DM, Galibert LJ, Maraskovsky E;  
XX WPI; 1998-377657/32.  
XX N-PSDB; AAV41379.  
PT New isolated ligand for receptor activator of NF-kappa B - used to  
PT develop products for augmenting an immune response for inhibiting an  
PT inflammatory response and for protection of cells.  
XX  
PS Example 14; Page 62-64; 80pp; English.  
XX This represents the murine muRANK (receptor activator of necrosis factor-  
CC kappaB (NF-kB)) polypeptide which is a homolog of the human RANK. RANK is  
CC a member of the tumour necrosis factor (TNF) family. A soluble RANK may  
CC be used for inhibiting activation of NF-kB, by contacting a cell  
CC expressing membrane-associated RANK with a soluble RANK which binds to  
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used  
CC to induce maturation of dendritic cells and enhance their allo-  
CC stimulatory capacity, thereby augmenting an immune response. The soluble  
CC RANK polypeptide composition may also be used for regulating an immune or  
CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be  
CC useful in ameliorating negative effects of an inflammatory response that  
CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,  
CC graft-versus-host reactions, or acute inflammatory reactions. They can  
CC also be used in adjunct therapy for disease characterised by neoplastic  
CC cells that express RANK. RANKL polypeptides can also be used to identify  
CC inhibitors of RANK and thus inhibitors of an inflammatory response, and  
CC also for protecting RANK-expressing cells from the negative effects of  
CC chemotherapy or the presence of high levels of TNF-alpha. The products  
CC can also be used for detection and drug screening  
XX  
SQ Sequence 625 AA;  
Query Match 15.1%; Score 215; DB 2; Length 625;  
Best Local Similarity 28.6%; Pred. No. 3e-09;  
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;  
QY 28 CDNCQPGTF-CRKNP-----VCKSCPSTF-SSIGQPNICRVACGYFRFKFCSSTH 81  
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKLLHKVCDAGKALVAVDPGNH 107  
QY 82 NA--ECECIEGFH-----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127  
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVF 164  
QY 128 NGTGVCPRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSIQV 186  
Db 165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSMTLRRPKEAQAYLPSLIV 217  
QY 187 LTLFLALTSALLLALIF-----ITLLFVLKWKIRKFFPHIFKQPFKKTGAQAQBEDA 238  
Db 218 LLLFISV--VVAAIIFGVYRKGGKALTANLWNWV-----NDA 254



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:35:32 ; Search time 36.8219 Seconds  
(without alignments)  
358.923 Million cell updates/sec

Title: US-10-067-122B-2  
Perfect score: 1428  
Sequence: 1 MGNNCYNVVIVLLVGCEK.....DACSRCRCPQEEGGGGYEL 256

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1428	100.0	256	1	US-08-236-918A-6 Sequence 6, Appli
2	1428	100.0	256	4	US-09-150-864A-6 Sequence 6, Appli
3	1428	100.0	256	4	US-08-012-269A-2 Sequence 2, Appli
4	1428	100.0	256	4	US-09-623-545A-3 Sequence 3, Appli
5	1428	100.0	256	5	PCT-US96-03965-2 Sequence 2, Appli
6	1085	76.0	191	3	US-08-974-022-52 Sequence 52, Appli
7	1085	76.0	191	3	US-08-795-445A-52 Sequence 52, Appli
8	1085	76.0	191	3	US-08-795-447A-52 Sequence 52, Appli
9	1085	76.0	191	3	US-08-974-186-52 Sequence 52, Appli
10	1085	76.0	191	3	US-08-795-446B-52 Sequence 52, Appli
11	1085	76.0	191	4	US-08-706-945D-139 Sequence 139, App
12	1085	76.0	191	4	US-08-577-788C-53 Sequence 53, Appli
13	795	55.7	255	1	US-08-236-918A-8 Sequence 8, Appli
14	795	55.7	255	2	US-08-816-605-9 Sequence 9, Appli
15	795	55.7	255	3	US-09-006-353A-11 Sequence 11, Appli
16	795	55.7	255	4	US-09-007-097-2 Sequence 2, Appli
17	795	55.7	255	4	US-09-150-864A-8 Sequence 8, Appli
18	795	55.7	255	4	US-09-573-986-11 Sequence 11, Appli
19	795	55.7	255	4	US-09-578-764A-2 Sequence 2, Appli
20	795	55.7	255	4	US-09-623-545A-2 Sequence 2, Appli
21	795	55.7	255	5	PCT-US96-03965-8 Sequence 8, Appli
22	656	45.9	219	2	US-08-816-605-2 Sequence 2, Appli
23	497	34.8	132	4	US-09-523-323-55 Sequence 55, Appli
24	268	18.8	69	3	US-08-866-545-11 Sequence 11, Appli
25	268	18.8	69	4	US-09-627-775-11 Sequence 11, Appli
26	237	16.6	415	3	US-09-006-353A-6 Sequence 6, Appli
27	237	16.6	415	4	US-09-573-986-6 Sequence 6, Appli

28	215	15.1	625	3	US-08-996-139-15	Sequence 15, Appli
29	215	15.1	625	3	US-08-995-659-15	Sequence 15, Appli
30	215	15.1	625	3	US-09-215-649A-15	Sequence 15, Appli
31	215	15.1	625	4	US-09-577-780-15	Sequence 15, Appli
32	215	15.1	625	4	US-09-577-800-15	Sequence 15, Appli
33	215	15.1	625	4	US-09-466-496-15	Sequence 15, Appli
34	215	15.1	625	4	US-09-871-856-15	Sequence 15, Appli
35	215	15.1	625	4	US-09-871-291-15	Sequence 15, Appli
36	215	15.1	625	4	US-09-877-650-15	Sequence 15, Appli
37	208.5	14.6	276	3	US-09-041-886-27	Sequence 27, Appli
38	208.5	14.6	277	3	US-09-042-785A-10	Sequence 10, Appli
39	208.5	14.6	277	3	US-09-006-353A-10	Sequence 10, Appli
40	208.5	14.6	277	4	US-08-114-944D-2	Sequence 2, Appli
41	208.5	14.6	277	4	US-09-573-986-10	Sequence 10, Appli
42	208.5	14.6	277	4	US-08-338-975A-2	Sequence 2, Appli
43	205.5	14.4	240	4	US-09-512-363-6	Sequence 6, Appli
44	205.5	14.4	240	4	US-09-176-200-6	Sequence 6, Appli
45	205.5	14.4	451	3	US-08-996-139-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-236-918A-6  
; Sequence 6, Application US/08236918A  
; Patent No. 5674704  
; GENERAL INFORMATION:  
; APPLICANT: Alderson, Mark R.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple 7.5.3  
; SOFTWARE: Microsoft Word, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,918A  
; FILING DATE: 06-May-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,843  
; FILING DATE: 07-May-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2801-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-236-918A-6

Query Match 100.0%; Score 1428; DB 1; Length 256;  
Best local Similarity 100.0%; Pred. No. 1e-118;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVVIVLLVGCEKVGAVQNSCNCQPGTFCRKNPVCVKSCPPSTFSSIGGQPN 60

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Db      1  MGNNCYNVVVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
QY      61  CNICRVACGYFRFKFCSSTHNAECIEGHCGLGPOCTRCCKDCRPGQELTKQGCKTCS 120
Db      61  CNICRVACGYFRFKFCSSTHNAECIEGHCGLGPOCTRCCKDCRPGQELTKQGCKTCS 120
QY      121  LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db      121  LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY      181  GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEEDACS 240
Db      181  GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEEDACS 240
QY      241  CRCPQEEEGGGGGYEL 256
Db      241  CRCPQEEEGGGGGYEL 256

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RESULT 2
US-09-150-864A-6
; Sequence 6, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; FILE OF INVENTION: That Binds Thereto
; FILE REFERENCE: 2801-B
; CURRENT APPLICATION NUMBER: US/09/150,864A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus sp. (clone: mu4-1BB)
US-09-150-864A-6

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Query Match      100.0%; Score 1428; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGNNCYNVVVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
Db      1  MGNNCYNVVVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
QY      61  CNICRVACGYFRFKFCSSTHNAECIEGHCGLGPOCTRCCKDCRPGQELTKQGCKTCS 120
Db      61  CNICRVACGYFRFKFCSSTHNAECIEGHCGLGPOCTRCCKDCRPGQELTKQGCKTCS 120
QY      121  LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db      121  LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY      181  GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEEDACS 240
Db      181  GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEEDACS 240
QY      241  CRCPQEEEGGGGGYEL 256
Db      241  CRCPQEEEGGGGGYEL 256

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RESULT 3
US-08-012-269A-2
; Sequence 2, Application US/08012269A
; Patent No. 6362325
; GENERAL INFORMATION:

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; APPLICANT: Kwon, Byoung S.
; TITLE OF INVENTION: MURINE 4-1BB GENE
; FILE REFERENCE: 740.009US1
; CURRENT APPLICATION NUMBER: US/08/012,269A
; CURRENT FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/922,996
; PRIOR FILING DATE: 1992-07-30
; PRIOR APPLICATION NUMBER: US 07/267,572
; PRIOR FILING DATE: 1988-11-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-012-269A-2

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Query Match      100.0%; Score 1428; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGNNCYNVVVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
Db      1  MGNNCYNVVVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
QY      61  CNICRVACGYFRFKFCSSTHNAECIEGHCGLGPOCTRCCKDCRPGQELTKQGCKTCS 120
Db      61  CNICRVACGYFRFKFCSSTHNAECIEGHCGLGPOCTRCCKDCRPGQELTKQGCKTCS 120
QY      121  LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db      121  LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
QY      181  GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEEDACS 240
Db      181  GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEEDACS 240
QY      241  CRCPQEEEGGGGGYEL 256
Db      241  CRCPQEEEGGGGGYEL 256

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RESULT 4
US-09-623-545A-3
; Sequence 3, Application US/09623545A
; Patent No. 6627200
; GENERAL INFORMATION:
; APPLICANT: Merckle GmbH
; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE
; FILE OF INVENTION: PROLIFERATION OF PERIPHERAL MONOCYTES
; FILE REFERENCE: 30424.1USWO
; CURRENT APPLICATION NUMBER: US/09/623,545A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: EPO 98103859.9
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/EP99/01440
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-623-545A-3

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Query Match      100.0%; Score 1428; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGNNCYNVVVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
Db      1  MGNNCYNVVVIVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60

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QY 61 CNICRVACGYFRFKKFCSSSTHNAECIEGFHCLGPOCTRCEKDCRPGQELTKQGCKTCS 120  
Db 61 CNICRVACGYFRFKKFCSSSTHNAECIEGFHCLGPOCTRCEKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLOVLTFLALTSALLALIFITLLFSLVKWIRKFPFHIFKQPFKKTGAQAQEDACS 240  
Db 181 GHSLOVLTFLALTSALLALIFITLLFSLVKWIRKFPFHIFKQPFKKTGAQAQEDACS 240  
QY 241 CRCPQEEEGGGGYEL 256  
Db 241 CRCPQEEEGGGGYEL 256

RESULT 5  
PCT-US96-03965-2  
; Sequence 2, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuil  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-1BB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KW05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-03965-2

Query Match 100.0%; Score 1428; DB 5; Length 256;  
Best Local Similarity 100.0%; Pred. No. 1e-118;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKNPVCCKSCPSTFSSIGGQPN 60  
Db 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKNPVCCKSCPSTFSSIGGQPN 60  
QY 61 CNICRVACGYFRFKKFCSSSTHNAECIEGFHCLGPOCTRCEKDCRPGQELTKQGCKTCS 120  
Db 61 CNICRVACGYFRFKKFCSSSTHNAECIEGFHCLGPOCTRCEKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLOVLTFLALTSALLALIFITLLFSLVKWIRKFPFHIFKQPFKKTGAQAQEDACS 240  
Db 181 GHSLOVLTFLALTSALLALIFITLLFSLVKWIRKFPFHIFKQPFKKTGAQAQEDACS 240  
QY 241 CRCPQEEEGGGGYEL 256  
Db 241 CRCPQEEEGGGGYEL 256

RESULT 6  
US-08-974-022-52  
; Sequence 52, Application US/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,022  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-974-022-52

Query Match 76.0%; Score 1085; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e-88;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKNPVCCKSCPSTFSSIGGQPN 60  
Db 1 MGNNCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKNPVCCKSCPSTFSSIGGQPN 60  
QY 61 CNICRVACGYFRFKKFCSSSTHNAECIEGFHCLGPOCTRCEKDCRPGQELTKQGCKTCS 120

Db 61 CNICRVAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLOVLTFL 191  
Db 181 GHSLOVLTFL 191

## RESULT 7

US-08-795-445A-52  
; Sequence 52, Application US/08795445A  
; Patent No. 6284485  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,445A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-795-445A-52

Query Match 76.0%; Score 1085; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e-88;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNNCYNVVVILLVGVCEKVGAVQNSCNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60  
Db 1 MGNNCYNVVVILLVGVCEKVGAVQNSCNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60  
QY 61 CNICRVAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
Db 61 CNICRVAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
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## RESULT 8

US-08-795-447A-52  
; Sequence 52, Application US/08795447A  
; Patent No. 6284728  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: One Amgen Center Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91362-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,447A  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378D2  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-795-447A-52

Query Match 76.0%; Score 1085; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e-88;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNCYNVVVILLVGVCEKVGAVQNSCNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60  
Db 1 MGNNCYNVVVILLVGVCEKVGAVQNSCNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60  
QY 61 CNICRVAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
Db 61 CNICRVAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLOVLTFL 191  
Db 181 GHSLOVLTFL 191

## RESULT 9

US-08-974-186-52  
; Sequence 52, Application US/08974186  
; Patent No. 6284740  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,186  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-186-52

Query Match 76.0%; Score 1085; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e-88;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFFSISGGQPN 60  
Db 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFFSISGGQPN 60  
QY 61 CNICRVAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQCKTCS 120  
Db 61 CNICRVAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLQVLTFL 191  
Db 181 GHSLQVLTFL 191

RESULT 10  
US-08-795-446B-52  
Sequence 52, Application US/08795446B  
Patent No. 6288032  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,446B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-446B-52

Query Match 76.0%; Score 1085; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e-88;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFFSISGGQPN 60  
Db 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFFSISGGQPN 60  
QY 61 CNICRVAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQCKTCS 120  
Db 61 CNICRVAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLQVLTFL 191  
Db 181 GHSLQVLTFL 191

RESULT 11  
US-08-706-945D-139  
Sequence 139, Application US/08706945D  
Patent No. 6369027  
GENERAL INFORMATION:  
APPLICANT: Boyle, William  
APPLICANT: Lacey, David  
APPLICANT: Calzone, Frank  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
FILE REFERENCE: A-378CIP  
CURRENT APPLICATION NUMBER: US/08/706,945D  
CURRENT FILING DATE: 1996-09-03  
PRIOR APPLICATION NUMBER: 08/577,788  
PRIOR FILING DATE: 1995-12-22  
NUMBER OF SEQ ID NOS: 145  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 139  
LENGTH: 191  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-706-945D-139

Query Match 76.0%; Score 1085; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e-88;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFFSISGGQPN 60  
Db 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFFSISGGQPN 60  
QY 61 CNICRVAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQCKTCS 120

Db 61 CNICRVAGYFRFKKFCSSTHNAECEIEGFHCLGPQCTCEKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLQVLTFL 191  
Db 181 GHSLQVLTFL 191

RESULT 12  
US-08-577-788C-53  
; Sequence 53, Application US/08577788C  
; Patent No. 6613544  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William  
; APPLICANT: Lacey, David  
; APPLICANT: Calzone, Frank  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; FILE REFERENCE: A-378 Rev  
; CURRENT APPLICATION NUMBER: US/08/577,788C  
; CURRENT FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-577-788C-53

Query Match 76.0%; Score 1085; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e-88;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCQPGTFCKKYNPVCKSCPPSTFSSIGGQPN 60  
Db 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCQPGTFCKKYNPVCKSCPPSTFSSIGGQPN 60  
QY 61 CNICRVAGYFRFKKFCSSTHNAECEIEGFHCLGPQCTCEKDCRPGQELTKQGCKTCS 120  
Db 61 CNICRVAGYFRFKKFCSSTHNAECEIEGFHCLGPQCTCEKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLQVLTFL 191  
Db 181 GHSLQVLTFL 191

RESULT 13  
US-08-236-918A-8  
; Sequence 8, Application US/08236918A  
; Patent No. 5674704  
; GENERAL INFORMATION:  
; APPLICANT: Alderson, Mark R.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple 7.5.3  
; SOFTWARE: Microsoft Word, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,918A  
; FILING DATE: 06-May-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,843  
; FILING DATE: 07-May-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2801-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-236-918A-8  
Query Match 55.7%; Score 795; DB 1; Length 255;  
Best Local Similarity 58.4%; Pred. No. 9.1e-63;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
QY 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCQPGTFCKKYNPVCKSCPPSTFSSIGGQPN 59  
Db 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCQPGTFCKKYNPVCKSCPPSTFSSIGGQPN 60  
QY 60 CNICRVAGYFRFKKFCSSTHNAECEIEGFHCLGPQCTCEKDCRPGQELTKQGCKTCS 119  
Db 61 TCDICRQCKGVFTRKECSSTNAECDCTPGFCHLGCSCMCEQDCKQGOELTKKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 179  
Db 121 CFGTFNDQK-RGICRPTNCSLDGKSVLVNGTKERDVVCGPSADLSPGAS-SVTTP-AP 177  
QY 180 G---GHSLQVLTFLALTS-ALLALIFITLLFSLVKWIRKFKPHFKQPFKKTGAQAE 235  
Db 178 AREPGHSPQIISFFALTSTALLFLFLLTFRFVVKRKKLLYIFKQPFMRPVQTQEQ 237  
QY 236 EDACSCRCPEEEGG 250  
Db 238 EDGCSRCPEEEEG 252

RESULT 14  
US-08-816-605-9  
; Sequence 9, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

Query Match 55.7%; Score 795; DB 3; Length 255;  
Best Local Similarity 58.4%; Pred. No. 9.1e-63;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

Qy	1	MGNNCYNVVVIVLLLVGCEKVGAVQNCSNCPQGTF-C-RKYNPVCKSPPPSTFSSIGGP	59
Dd	1	MGNSCYNIVATLLLVNLNFERTRSLQDPCSNCPAGTFCDDNNRNQICSPCPPNSPSSAGGR	60
Qy	60	NCNICRYCAGYFRFFKFCSSSTHNABECIEGFHCLGPQCTRCEKDRCRPGQELTKQGCKTC	119
Dd	61	TCDICROCKGVFTRKECSSSTNAECDCTPGFHCLGAGCSMCEQDKCKQGLTKKGCKDC	120
Qy	120	SLGTENDONGTVCRPWNTCSLDGRSVLKTGTTEKDVCGPPVVSFSSTTISVTPEGGP	179
Dd	121	CFGTFNDOK-RGICRPWNTCSLDGKSVLVNGTKERDVCGGPSPADLSPGAS-SVTPP-AP	177
Qy	180	G---GHSLQVLTLFLALTS-ALLLALIFITLLFSVLKWIRKKFPPIFKOPFKKTTGAAQE	235
Dd	178	AREPGHSPIIISFFLALTSTALLFLFLFTLRFSVVRGRKKLLYIFXQPFMRPVQTTOE	237
Qy	236	EDACSCRCPQEEEGG	250
Dd	238	EDGCSCRFPEEEEGG	252

```

RESULT 16
US-09-007-097-2
; Sequence 2, Application US/09007097A
; Patent No. 6303121
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/007,097A
; CURRENT FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-007-097-2

```

[illegible]



CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,796  
FILING DATE: 16-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,269  
FILING DATE: 01-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,996  
FILING DATE: 30-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/267,577  
FILING DATE: 07-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A  
REGISTRATION NUMBER: 34,390  
REFERENCE/DOCKET NUMBER: KMOS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03965-8

Query Match 55.7%; Score 795; DB 5; Length 255;  
Best Local Similarity 58.4%; Pred. No. 9.1e-63;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
QY 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
QY 60 NCNCRVCAGYFRFKKFCSSSTHNAECIEGFCGLGPGCTRCCKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFHCGLGAGCSMCEQDCKQGLTKKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVCGPSPADLSPGAS-SVTPP-AP 177  
QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSLVKWIRKKFPHIFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVKGRKKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPOEEGG 250  
Db 238 EDGCSRCRFPPEEGG 252

RESULT 22  
US-08-816-605-2  
Sequence 2, Application US/08816605  
Patent No. 5874240  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Gentz, Reiner  
TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

RESULT 20  
US-09-623-545A-2  
Sequence 2, Application US/09623545A  
Patent No. 6627200  
GENERAL INFORMATION:  
APPLICANT: Merckle GmbH  
TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE  
PROLIFERATION OF PERIPHERAL MONOCYTES  
FILE REFERENCE: 30424.1USWO  
CURRENT APPLICATION NUMBER: US/09/623,545A  
CURRENT FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: EPO 98103859.9  
PRIOR FILING DATE: 1999-03-05  
PRIOR APPLICATION NUMBER: PCT/EP99/01440  
PRIOR FILING DATE: 1999-03-05  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-623-545A-2

Query Match 55.7%; Score 795; DB 4; Length 255;  
Best Local Similarity 58.4%; Pred. No. 9.1e-63;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
QY 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
QY 60 NCNCRVCAGYFRFKKFCSSSTHNAECIEGFCGLGPGCTRCCKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFHCGLGAGCSMCEQDCKQGLTKKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVCGPSPADLSPGAS-SVTPP-AP 177  
QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSLVKWIRKKFPHIFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLTLRFSVVKGRKKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPOEEGG 250  
Db 238 EDGCSRCRFPPEEGG 252

RESULT 21  
PCT-US96-03965-8  
Sequence 8, Application PC/TUS9603965  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung Se  
APPLICANT: Kang, Chang-Yuil  
TITLE OF INVENTION: Monoclonal antibody against human  
TITLE OF INVENTION: receptor 4-1BB  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Barnard, Brown & Michaels  
STREET: 306 East State Street, Suite 220  
CITY: Ithaca  
STATE: NY  
COUNTRY: USA  
ZIP: 14850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03965  
FILING DATE:

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,605  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-816-605-2

Query Match 45.9%; Score 656; DB 2; Length 219;  
Best Local Similarity 51.2%; Pred. No. 1.5e-50;  
Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;  
QY 1 MGNVCYNVIVVILLVGCXKVGAVQNSCDNCQPGTFCKKYNPVCKSCPSTFSSIGGQPN 60  
Db 1 MGNVCYNVIVVILLVGCXKVGAVQNSCDNCQPGTFCKKYNPVCKSCPSTFSSIGGQPN 60  
QY 61 CNICRVACAGYFRFKKFCSSSTHNAECCIEGFHCLGPOCTRCEKDCRPGQELTKQCKTCS 120  
Db 33 -----AGVTRTRKECSSTSNACEDCTFGHCLGAGCSMCEQDCKQGLTKKGCXDC 85  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGPG 180  
Db 86 FGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSFGAS-SVTTP-APA 142  
QY 181 ---GHSQVLTFLALTS-ALLLALIFITLLFSVLKWKIRKFFPHIFKQPFKTTGAQEE 236  
Db 143 REPCHSPQIISFFLALTSALLFLFLFTRFSVVRGRKKLLYIFKQPFMRPVQTTQEE 202  
QY 237 DACSCRCPOEEGG 250  
Db 203 DGCSCRFPPEEG 216

RESULT 23  
US-09-523-323-55  
Sequence 55, Application US/09523323  
Patent No. 6635743  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.  
APPLICANT: Ullrich, Stephen  
APPLICANT: Zhai, Yifan  
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
FILE REFERENCE: 1488.065000C  
CURRENT APPLICATION NUMBER: US/09/523,323  
CURRENT FILING DATE: 2000-03-10  
EARLIER APPLICATION NUMBER: 60/168,380  
EARLIER FILING DATE: 1999-12-02  
EARLIER APPLICATION NUMBER: 60/148,326  
EARLIER FILING DATE: 1999-08-11  
EARLIER APPLICATION NUMBER: 60/142,657  
EARLIER FILING DATE: 1999-07-06  
EARLIER APPLICATION NUMBER: 60/137,457  
EARLIER FILING DATE: 1999-06-04  
EARLIER APPLICATION NUMBER: 60/124,041  
EARLIER FILING DATE: 1999-03-11  
EARLIER APPLICATION NUMBER: 09/252,656  
EARLIER FILING DATE: 1999-02-19  
EARLIER APPLICATION NUMBER: 60/075,409

EARLIER FILING DATE: 1998-02-20  
EARLIER APPLICATION NUMBER: 09/027,287  
EARLIER FILING DATE: 1998-02-20  
EARLIER APPLICATION NUMBER: 09/003,886  
EARLIER FILING DATE: 1998-01-07  
EARLIER APPLICATION NUMBER: 08/822,953  
EARLIER FILING DATE: 1997-03-21  
EARLIER APPLICATION NUMBER: 60/013,923  
EARLIER FILING DATE: 1996-03-22  
EARLIER APPLICATION NUMBER: 60/030,157  
EARLIER FILING DATE: 1996-10-31  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 55  
LENGTH: 132  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-523-323-55

Query Match 34.8%; Score 497; DB 4; Length 132;  
Best Local Similarity 63.9%; Pred. No. 9.6e-37;  
Matches 85; Conservative 13; Mismatches 33; Indels 2; Gaps 2;  
QY 28 CDNCQPGTFCR-KYNPVCKSCPSTFSSIGGQPNICRVACAGYFRFKKFCSSSTHNAECC 86  
Db 1 CSNCPAGTFCDWNRNQICSPCPNPSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNACD 60  
QY 87 CIEGFHCLGPOCTRCEKDCRPGQELTKQCKTCSLGTENDQNGTGVCRPWTNCSLDGRSV 146  
Db 61 CTPGFHCLGAGCSMCEQDCKQGLTKKGCXDCCTFGHCLGAGCSMCEQDCKQGLTKKGCXDC 119  
QY 147 LKGTTEKDVVCG 159  
Db 120 LVNGTKERDVVCG 132

RESULT 24  
US-08-866-545-11  
Sequence 11, Application US/08866545  
Patent No. 6265535  
GENERAL INFORMATION:  
APPLICANT: Greene, Mark I.  
APPLICANT: Murali, Ramachandran  
APPLICANT: Takasaki, Wataru  
TITLE OF INVENTION: PEPTIDES AND PEPTIDE  
TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR  
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR  
TITLE OF INVENTION: USES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/866,545  
FILING DATE: 30-MAY-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009113-0004-999  
TELECOMMUNICATION INFORMATION:

RESULT 27  
US-09-573-986-6  
; Sequence 6, Application US/09573986  
; Patent No. 6455040  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.128000/4  
; CURRENT APPLICATION NUMBER: US/09/573,986  
; CURRENT FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 415

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-6

Query Match      16.6%; Score 237; DB 4; Length 415;
Best Local Similarity 27.0%; Pred. No. 3.3e-13;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCQPGTF-----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVACGYFRFKF--CSS 79
Db 59 CSRCPGGEFVFAVCSRSQDTVCKTCPHNSYNEHWNHLSLTCQLCRPCDIVLGFEEVAPCTS 118
QY 80 THNAECECIEGHC--LGPOCTRCEKD-----CRPGQEL-----TKQGCKTCSLGTGTF- 124
Db 119 DRKAECRCQPMSCVYLDNECVHCEERLVLCQPGTEABVTDEIMDTDVCVPCKEGHFQ 178
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGCHSL 184
Db 179 NTSSPRARQPHTRCEIQGLVEAAPGTSYSDTICKNP-----PEPG----- 219
QY 185 QVTLFLALTSALLLALIFITLLFSLVKWIR-----KKFPHIFKQPFKKTGTGAQAQBEDAC 239
Db 220 --AMLLALLLSLVLFLETTVL--ACAWMRHPSLCRLGLTLLKR-----HPGEES 268
QY 240 SCRCPOEE 247
Db 269 PCPAPRAD 276

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RESULT 28
US-08-996-139-15
; Sequence 15, Application US/08996139
; Patent No. 601729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-15

Query Match      15.1%; Score 215; DB 3; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VCKSCPPSTF-SSIGGQPNICRVACGYFRFKKFCSTH 81
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECECIEGHC--CLGPOCTRCEKDCRPG-----QELTKQG-CKTCSLGTGTFNDQ- 127
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAQHPLQLNKDVTCTPCLLGGFFSDVF 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLQV 186
Db 165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSMTLRRPPEKAQAYLPSLIV 217
QY 187 LTLFLALTSALLLALIF-----ITLLFSLVKWIRKFPFHIFKQPFKKTGTGAQAQBEDA 238
Db 218 LLLFISV--VVVAAIIFGVYRKGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEEGG 250
Db 255 CSSLSGNKESG 266

```

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RESULT 29
US-08-995-659-15
; Sequence 15, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Power Macintosh
; SOFTWARE: Apple Operating System 7.5.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A

```

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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 625 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-995-659-15

Query Match      15.1%; Score 215; DB 3; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCPGTF-CRKNP-----VCKSCPSTF-SSIGQPNCNICRVACAGYFRFKKFCSTH 81
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECECIEGFH----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAQLPLQLNKDTVCTPCLLGFFSDVF 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186
Db 165 SSTDKCKPWTNCTLLGKLEAHQGTESDVVC-----SSMTLRRPPKEAQAYLPSLIV 217
QY 187 LTLFLALTSALLLALIF-----ITLLFVLKWKIRKFFPHFKQPFKTTGAAQEEDA 238
Db 218 LLLFISV--VVAAIIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEEG 250
Db 255 CSSLSGNKSSG 266

RESULT 30
US-09-215-649A-15
; Sequence 15, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,649A
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
```

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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 625 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-215-649A-15

Query Match      15.1%; Score 215; DB 3; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCPGTF-CRKNP-----VCKSCPSTF-SSIGQPNCNICRVACAGYFRFKKFCSTH 81
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECECIEGFH----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAQLPLQLNKDTVCTPCLLGFFSDVF 164
QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186
Db 165 SSTDKCKPWTNCTLLGKLEAHQGTESDVVC-----SSMTLRRPPKEAQAYLPSLIV 217
QY 187 LTLFLALTSALLLALIF-----ITLLFVLKWKIRKFFPHFKQPFKTTGAAQEEDA 238
Db 218 LLLFISV--VVAAIIFGVYRKGGKALTANLWNV-----NDA 254
QY 239 CSCRCPOEEEG 250
Db 255 CSSLSGNKSSG 266

RESULT 31
US-09-577-780-15
; Sequence 15, Application US/09577780
; Patent No. 6419929
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,780
; FILING DATE: 24-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
```

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REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-780-15

Query Match 15.1%; Score 215; DB 4; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKYNP-----VKSCPPSTF-SSIGQPNICRVACAGYFRFKFCSSTH 81
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECEIEGFH---CLGPOCTRCEKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVF 164
QY 128 NGTGVCPRWNTCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186
Db 165 SSTDKCKPWNTCTLLGLEAHQGTSDVVC-----SSMTLRRPPKEAQAYLPSLIV 217
QY 187 LTLFLALTSALLLALIF-----ITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEDA 238
Db 218 LLLFISV--VVAAIIFGVYRKGGKALTANLWNWV-----NDA 254
QY 239 CSCRCPOEEGG 250
Db 255 CSSLSGNKESSG 266

RESULT 32
US-09-577-800-15
Sequence 15, Application US/09577800
Patent No. 6479635
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,800
FILING DATE: 24-MAY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/996,139
FILING DATE: 22 DECEMBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997

REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-800-15

Query Match 15.1%; Score 215; DB 4; Length 625;
Best Local Similarity 28.6%; Pred. No. 4.6e-11;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKYNP-----VKSCPPSTF-SSIGQPNICRVACAGYFRFKFCSSTH 81
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107
QY 82 NA--ECEIEGFH---CLGPOCTRCEKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVF 164
QY 128 NGTGVCPRWNTCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186
Db 165 SSTDKCKPWNTCTLLGLEAHQGTSDVVC-----SSMTLRRPPKEAQAYLPSLIV 217
QY 187 LTLFLALTSALLLALIF-----ITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEDA 238
Db 218 LLLFISV--VVAAIIFGVYRKGGKALTANLWNWV-----NDA 254
QY 239 CSCRCPOEEGG 250
Db 255 CSSLSGNKESSG 266

RESULT 33
US-09-466-496-15
Sequence 15, Application US/09466496
Patent No. 6528482
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/466,496
FILING DATE: 17-DEC-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
APPLICATION NUMBER: USSN 60/064,671
```

FILING DATE: 14 OCTOBER 1997  
 APPLICATION NUMBER: USSN 08/813,509  
 FILING DATE: 07 MARCH 1997  
 APPLICATION NUMBER: USSN 08/772,330  
 FILING DATE: 23 DECEMBER 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2851-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)233-0644  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 625 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 US-09-466-496-15

Query Match 15.1%; Score 215; DB 4; Length 625;  
 Best Local Similarity 28.6%; Pred. No. 4.6e-11;  
 Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VCKSCPSTF-SSIGQPNICRVACGYFRFKKFCSTH 81  
 Db 48 CSRCEPKYLSSKCTPTSDSVCLPCGDEYLDTWNEEDKLLHKVCDAGKALVAVDPGNH 107

QY 82 NA--ECECIEGFH-----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTFTNDQ- 127  
 Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAQHPLQNLKDTVCTPCLLGGFFSDVF 164

QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186  
 Db 165 SSTDKCKPWTNCTLLGKLEAHQGTESDVVC-----SSMTLRRPPKEAQAYLPSLIV 217

QY 187 LTLFLALTSALLLALIF-----ITLLFSVLKWKRPKPHIFKQPFKKTGTGAQEEEDA 238  
 Db 218 LLLFISV--VVVAAILFGVYVRKGGKALTANLWNV-----NDA 254

QY 239 CSCRCPEEEGG 250  
 Db 255 CSSLSGNKSSG 266

RESULT 34  
 US-09-871-856-15  
 ; Sequence 15, Application US/09871856  
 ; Patent No. 6537763  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Dirk M.  
 ; Galibert, Laurent  
 ; Maraskovsky, Eugene  
 ; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation, Law Department  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/871,856  
 ; FILING DATE: 31-May-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: USSN 08/813,509  
 FILING DATE: 07 MARCH 1997  
 APPLICATION NUMBER: USSN 08/772,330  
 FILING DATE: 23 DECEMBER 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2851-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)233-0644  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 625 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 US-09-871-856-15

Query Match 15.1%; Score 215; DB 4; Length 625;  
 Best Local Similarity 28.6%; Pred. No. 4.6e-11;  
 Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VCKSCPSTF-SSIGQPNICRVACGYFRFKKFCSTH 81  
 Db 48 CSRCEPKYLSSKCTPTSDSVCLPCGDEYLDTWNEEDKLLHKVCDAGKALVAVDPGNH 107

QY 82 NA--ECECIEGFH-----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTFTNDQ- 127  
 Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAQHPLQNLKDTVCTPCLLGGFFSDVF 164

QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186  
 Db 165 SSTDKCKPWTNCTLLGKLEAHQGTESDVVC-----SSMTLRRPPKEAQAYLPSLIV 217

QY 187 LTLFLALTSALLLALIF-----ITLLFSVLKWKRPKPHIFKQPFKKTGTGAQEEEDA 238  
 Db 218 LLLFISV--VVVAAILFGVYVRKGGKALTANLWNV-----NDA 254

QY 239 CSCRCPEEEGG 250  
 Db 255 CSSLSGNKSSG 266

RESULT 35  
 US-09-871-291-15  
 ; Sequence 15, Application US/09871291  
 ; Patent No. 6562948  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Dirk M.  
 ; Galibert, Laurent  
 ; Maraskovsky, Eugene  
 ; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation, Law Department  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/871,291  
 ; FILING DATE: 30-May-2001  
 ; CLASSIFICATION: <Unknown>







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:40:42 ; Search time 94.6849 Seconds  
(without alignments)  
749.438 Million cell updates/sec

Title: US-10-067-122B-2  
Perfect score: 1428  
Sequence: 1 MGNNCYNVVVILLVGCEK.....DACSCRCQEBEGGGGYEL 256

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1428	100.0	256	13	US-10-027-199-10
2	1428	100.0	256	14	US-10-067-122-2
3	1085	76.0	191	11	US-09-405-032-136
4	795	55.7	255	9	US-09-739-394-9
5	795	55.7	255	9	US-09-826-212-11
6	795	55.7	255	9	US-09-935-727-13
7	795	55.7	255	10	US-09-877-336-2
8	795	55.7	255	13	US-10-097-330-9
9	795	55.7	255	13	US-10-027-199-2
10	795	55.7	255	14	US-10-170-997-2
11	795	55.7	255	14	US-10-186-643-11
12	795	55.7	255	14	US-10-207-655-160
13	795	55.7	255	15	US-10-418-242-13
14	656	45.9	219	9	US-09-739-394-2
15	656	45.9	219	13	US-10-097-330-2

16	497	34.8	132	15	US-10-375-680-55	Sequence 55, Appl
17	237	16.6	402	12	US-10-087-192-939	Sequence 939, Appl
18	237	16.6	415	9	US-09-826-212-6	Sequence 6, Appli
19	237	16.6	415	9	US-09-907-372-20	Sequence 20, Appl
20	237	16.6	415	9	US-09-935-727-8	Sequence 8, Appli
21	237	16.6	415	10	US-09-917-372-20	Sequence 20, Appl
22	237	16.6	415	14	US-10-186-643-6	Sequence 6, Appli
23	237	16.6	415	15	US-10-418-242-8	Sequence 8, Appli
24	215	15.1	625	9	US-09-871-856-15	Sequence 15, Appl
25	215	15.1	625	9	US-09-877-650-15	Sequence 15, Appl
26	215	15.1	625	12	US-09-865-363-15	Sequence 15, Appl
27	215	15.1	625	12	US-10-151-071-2	Sequence 2, Appli
28	215	15.1	625	12	US-09-957-944-4	Sequence 4, Appli
29	215	15.1	625	14	US-10-166-232A-2	Sequence 2, Appli
30	215	15.1	625	14	US-10-405-878-15	Sequence 15, Appl
31	214.5	15.0	277	9	US-09-839-339A-1	Sequence 1, Appli
32	212.5	14.9	276	15	US-10-369-300-4	Sequence 4, Appli
33	209.5	14.7	615	9	US-09-768-779A-2	Sequence 2, Appli
34	209.5	14.7	615	14	US-10-291-480-2	Sequence 10, Appl
35	208.5	14.6	277	9	US-09-826-212-10	Sequence 2, Appli
36	208.5	14.6	277	9	US-09-768-779A-4	Sequence 4, Appli
37	208.5	14.6	277	9	US-09-935-727-12	Sequence 12, Appl
38	208.5	14.6	277	12	US-10-328-953-323	Sequence 323, App
39	208.5	14.6	277	14	US-10-291-480-4	Sequence 4, Appli
40	208.5	14.6	277	14	US-10-186-643-10	Sequence 10, Appl
41	208.5	14.6	277	15	US-10-418-242-12	Sequence 12, Appl
42	207.5	14.5	277	9	US-09-855-528-2	Sequence 2, Appli
43	206	14.4	622	12	US-09-957-944-10	Sequence 10, Appl
44	205.5	14.4	240	9	US-09-915-593-6	Sequence 6, Appli
45	205.5	14.4	240	14	US-10-283-105-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-10-027-199-10  
; Sequence 10, Application US/10027199  
; Publication No. US20020168719A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung  
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND METHODS  
; FILE REFERENCE: 740.013US2  
; CURRENT APPLICATION NUMBER: US/10/027,199  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-10-22  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1995-06-05  
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1993-09-03  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-027-199-10

Query Match 100.0%; Score 1428; DB 13; Length 256;  
Best Local Similarity 100.0%; Pred. No. 4.6e-119;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGNNCYNVVVILLVGCEKYGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
DB	1	MGNNCYNVVVILLVGCEKYGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN 60
QY	61	CNCRVCAGYFRFKFCSSSTHNAECEIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120
DB	61	CNCRVCAGYFRFKFCSSSTHNAECEIEGFHCLGPQCTRCEKDCRPGQELTKQGCKTCS 120
QY	121	LGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180

Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFFHIFKQPFKKTGTGAQEEEDACS 240  
Db 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFFHIFKQPFKKTGTGAQEEEDACS 240  
QY 241 CRCPQEEEGGGGYEL 256  
Db 241 CRCPQEEEGGGGYEL 256

RESULT 2

US-10-067-122-2  
; Sequence 2, Application US/10067122  
; Publication No. US20030100745A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung S.  
; TITLE OF INVENTION: MURINE 4-1BB GENE  
; FILE REFERENCE: 740.009US1  
; CURRENT APPLICATION NUMBER: US/10/067,122  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 08/012,269  
; PRIOR FILING DATE: 1993-02-01  
; PRIOR APPLICATION NUMBER: US 07/922,996  
; PRIOR FILING DATE: 1992-07-30  
; PRIOR APPLICATION NUMBER: US 07/267,572  
; PRIOR FILING DATE: 1988-11-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-067-122-2

Query Match 100.0%; Score 1428; DB 14; Length 256;  
Best Local Similarity 100.0%; Pred. No. 4.6e-119;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNVCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60  
Db 1 MGNVCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60  
QY 61 CNICRVAGYFRFKFCSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
Db 61 CNICRVAGYFRFKFCSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFFHIFKQPFKKTGTGAQEEEDACS 240  
Db 181 GHSLOVLTFLALTSALLLALIFITLLFSVLKWKIRKFFHIFKQPFKKTGTGAQEEEDACS 240  
QY 241 CRCPQEEEGGGGYEL 256  
Db 241 CRCPQEEEGGGGYEL 256

RESULT 3

US-09-405-032-136  
; Sequence 136, Application US/09405032  
; Publication No. US20030207827A1  
; GENERAL INFORMATION:  
; APPLICANT: Amgen Inc.  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 168  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks

; STATE: California  
; COUNTRY: United States  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/405,032  
; FILING DATE: 24-Sep-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378-CIP2  
; INFORMATION FOR SEQ ID NO: 136:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 136:  
US-09-405-032-136

Query Match 76.0%; Score 1085; DB 11; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.1e-88;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNVCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60  
Db 1 MGNVCYNVVVIVLLLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPSTFSSIGGQPN 60  
QY 61 CNICRVAGYFRFKFCSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
Db 61 CNICRVAGYFRFKFCSSTHNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120  
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
Db 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180  
QY 181 GHSLOVLTFL 191  
Db 181 GHSLOVLTFL 191

RESULT 4

US-09-739-394-9  
; Sequence 9, Application US/09739394  
; Patent No. US2001001465A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; Yu, Guo-Liang  
; Gentz, Reiner  
; TITLE OF INVENTION: Human 4-1BB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/739,394  
; FILING DATE: 19-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/253,549  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-739-394-9

Query Match 55.7%; Score 795; DB 9; Length 255;  
Best Local Similarity 58.4%; Pred. No. 1e-62;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCYNVAVVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNNSYNIVATLLVLNFERTRSLQDPCSNCPAGTFCDDNRNQCPCPPNSFSSAGGQR 60  
QY 60 NCNCRVCAGYFRFKKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTSNACDCTPGFHCLGAGCSMCEQDCKQGGELTKKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTPP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFHFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIISFFLALTSTALLFLLFLLTRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPEEEGG 250  
Db 238 EDGCSRCRPEEEGG 252

RESULT 5  
US-09-826-212-11  
Sequence 11, Application US/09826212  
Patent No. US20010021516A1  
GENERAL INFORMATION:  
APPLICANT: Wei, Ying-Fei  
APPLICANT: Gentz, Reiner  
APPLICANT: Ruben, Steven  
APPLICANT: Ni, Jian  
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
FILE REFERENCE: 1488.128006  
CURRENT APPLICATION NUMBER: US/09/826,212  
CURRENT FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-826-212-11

Query Match 55.7%; Score 795; DB 9; Length 255;  
Best Local Similarity 58.4%; Pred. No. 1e-62;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCYNVAVVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNNSYNIVATLLVLNFERTRSLQDPCSNCPAGTFCDDNRNQCPCPPNSFSSAGGQR 60

QY 60 NCNCRVCAGYFRFKKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTSNACDCTPGFHCLGAGCSMCEQDCKQGGELTKKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTPP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFFHFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIISFFLALTSTALLFLLFLLTRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPEEEGG 250  
Db 238 EDGCSRCRPEEEGG 252

RESULT 6  
US-09-935-727-13  
Sequence 13, Application US/09935727  
Patent No. US20020150583A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
FILE REFERENCE: PF454P2  
CURRENT APPLICATION NUMBER: US/09/935,727  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 60/303,224  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: 60/252,131  
PRIOR FILING DATE: 2000-11-21  
PRIOR APPLICATION NUMBER: 60/227,598  
PRIOR FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: 09/518,931  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: 60/168,235  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 60/146,371  
PRIOR FILING DATE: 1999-08-02  
PRIOR APPLICATION NUMBER: 60/131,964  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: 60/131,270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/124,092  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/121,774  
PRIOR FILING DATE: 1999-03-04  
PRIOR APPLICATION NUMBER: 09/006,352  
PRIOR FILING DATE: 1998-01-13  
PRIOR APPLICATION NUMBER: 60/035,496  
PRIOR FILING DATE: 1997-01-14  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-935-727-13

Query Match 55.7%; Score 795; DB 9; Length 255;  
Best Local Similarity 58.4%; Pred. No. 1e-62;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCYNVAVVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNNSYNIVATLLVLNFERTRSLQDPCSNCPAGTFCDDNRNQCPCPPNSFSSAGGQR 60  
QY 60 NCNCRVCAGYFRFKKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTSNACDCTPGFHCLGAGCSMCEQDCKQGGELTKKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179

Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNFKTRDGVVCGSPADLSPGAS-SVTPP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKFFPHIFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLFRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPEEEGG 250  
Db 238 EDGCSRCRFEEEGG 252

## RESULT 7

US-09-877-336-2  
; Sequence 2, Application US/09877336  
; Publication No. US20030000851A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung  
; TITLE OF INVENTION: METHODS OF USING HUMAN RECEPTOR ON  
; FILE REFERENCE: 740.011US3  
; CURRENT APPLICATION NUMBER: US/09/877,336  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: 09/007,097  
; PRIOR FILING DATE: 1998-01-14  
; PRIOR APPLICATION NUMBER: 08/409,851  
; PRIOR FILING DATE: 1995-03-23  
; PRIOR APPLICATION NUMBER: 08/122,796  
; PRIOR FILING DATE: 1993-09-16  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-877-336-2

Query Match 55.7%; Score 795; DB 10; Length 255;  
Best Local Similarity 58.4%; Pred. No. 1e-62;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCYNVVVVILLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNSCYNIVATLLLVNFRTRSLQDPCSNCPAGTFCNDRNRNQICSPCPNSFSAGGQR 60  
QY 60 NCNCRVCAGYFRFKFCSTHNAECEIEGFCGLGPOCTRCCKRPGQELTKGCKTC 119  
Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFCHLGCAGCSMCEQDCKQGLTKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNFKTRDGVVCGSPADLSPGAS-SVTPP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKFFPHIFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLFRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPEEEGG 250  
Db 238 EDGCSRCRFEEEGG 252

## RESULT 8

US-10-097-330-9  
; Sequence 9, Application US/10097330  
; Publication No. US20020127651A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT  
; FILE REFERENCE: PF254D1C2  
; CURRENT APPLICATION NUMBER: US/10/097,330  
; CURRENT FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 09/739,394  
; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: US 09/253,549  
; PRIOR FILING DATE: 1999-02-22  
; PRIOR APPLICATION NUMBER: US 08/816,605  
; PRIOR FILING DATE: 1997-03-13  
; PRIOR APPLICATION NUMBER: US 60/013,474  
; PRIOR FILING DATE: 1996-03-15  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-097-330-9

Query Match 55.7%; Score 795; DB 13; Length 255;  
Best Local Similarity 58.4%; Pred. No. 1e-62;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCYNVVVVILLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNSCYNIVATLLLVNFRTRSLQDPCSNCPAGTFCNDRNRNQICSPCPNSFSAGGQR 60  
QY 60 NCNCRVCAGYFRFKFCSTHNAECEIEGFCGLGPOCTRCCKRPGQELTKGCKTC 119  
Db 61 TCDICRQCKGVFRTRKESSTNAECDCTPGFCHLGCAGCSMCEQDCKQGLTKGCKDC 120  
QY 120 SLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNFKTRDGVVCGSPADLSPGAS-SVTPP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKFFPHIFKQPFKKTGAAQE 235  
Db 178 AREPGHSPQIIISFFLALTSTALLFLFLFRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPEEEGG 250  
Db 238 EDGCSRCRFEEEGG 252

## RESULT 9

US-10-027-199-2  
; Sequence 2, Application US/10027199  
; Publication No. US20020168719A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung  
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND  
; METHODS  
; FILE REFERENCE: 740.013US2  
; CURRENT APPLICATION NUMBER: US/10/027,199  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652  
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/122,796  
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-027-199-2

Query Match 55.7%; Score 795; DB 13; Length 255;  
Best Local Similarity 58.4%; Pred. No. 1e-62;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCYNVVVVILLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNSCYNIVATLLLVNFRTRSLQDPCSNCPAGTFCNDRNRNQICSPCPNSFSAGGQR 60  
QY 60 NCNCRVCAGYFRFKFCSTHNAECEIEGFCGLGPOCTRCCKRPGQELTKGCKTC 119

Db 61 TCDICRQCKGVFRTRKECSSTNAECDCPTGFHCLGAGCSMCEQDCKQQLTKKGCKDC 120  
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPPHIFKQPFKKTGAQAE 235  
Db 178 AREPGHSPQIISFFLALTSTALLFLFLTLRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPOEEEG 250  
Db 238 EDGSCRFPEEEEG 252

RESULT 10  
US-10-170-997-2  
; Sequence 2, Application US/10170997  
; Publication No. US20030082157A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; TITLE OF INVENTION: New Receptor and Related Products and Methods  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/170,997  
; FILING DATE: 12-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/955,573  
; FILING DATE: 22-OCT-1997  
; APPLICATION NUMBER: 08/460,976  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/122,796  
; FILING DATE: 13-SEP-1993  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; APPLICATION NUMBER: US 08/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KWO4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-170-997-2

Query Match 55.7%; Score 795; DB 14; Length 255;  
Best Local Similarity 58.4%; Pred. No. 1e-62;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNSCYNIVATLLLVNFERTRSLQDPCSNCPAGTFCDDNRNQICSPCPNPSFSSAGGQR 60  
QY 60 NCNIRVCAGYFRFKFCSSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKQCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTNAECDCPTGFHCLGAGCSMCEQDCKQQLTKKGCKDC 120  
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPPHIFKQPFKKTGAQAE 235  
Db 178 AREPGHSPQIISFFLALTSTALLFLFLTLRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPOEEEG 250  
Db 238 EDGSCRFPEEEEG 252

RESULT 11  
US-10-186-643-11  
; Sequence 11, Application US/10186643  
; Publication No. US20030118546A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.1280004  
; CURRENT APPLICATION NUMBER: US/10/186,643  
; CURRENT FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: US/09/573,986  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-186-643-11

Query Match 55.7%; Score 795; DB 14; Length 255;  
Best Local Similarity 58.4%; Pred. No. 1e-62;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCYNVWVIVLLVGCCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59  
Db 1 MGNSCYNIVATLLLVNFERTRSLQDPCSNCPAGTFCDDNRNQICSPCPNPSFSSAGGQR 60  
QY 60 NCNIRVCAGYFRFKFCSSSTHNAECIEGFHCLGPOCTRCCKDCRPGQELTKQCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTNAECDCPTGFHCLGAGCSMCEQDCKQQLTKKGCKDC 120  
QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 121 CFGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTTP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSVLKWKIRKPPHIFKQPFKKTGAQAE 235  
Db 178 AREPGHSPQIISFFLALTSTALLFLFLTLRFSVVKRGRKLLYIFKQPFMRPVQTTQE 237  
QY 236 EDACSCRCPOEEEG 250  
Db 238 EDGSCRFPEEEEG 252

RESULT 12  
US-10-207-655-160  
; Sequence 160, Application US/10207655

Publication No. US20030118592A1  
 GENERAL INFORMATION:  
 APPLICANT: Ledbetter, Jeffrey A.  
 APPLICANT: Hayden-Ledbetter, Martha S.  
 TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
 FILE REFERENCE: 390069.401C1  
 CURRENT APPLICATION NUMBER: US/10/207,655  
 CURRENT FILING DATE: 2002-07-25  
 NUMBER OF SEQ ID NOS: 426  
 SOFTWARE: PatentIn version 3.0

SEQ ID NO 160  
 LENGTH: 255  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-207-655-160

Query Match 55.7%; Score 795; DB 14; Length 255;  
 Best Local Similarity 58.4%; Pred. No. 1e-62;  
 Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
 QY 1 MGNVCYNVVIVLLVGVCEKVGAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGQP 59  
 Db 1 MGNVCYNIVATLLVLFNFRTRSLQDPCSNCPAGTFCDNRRNQICSPCPNPSFSSAGGQ 60  
 QY 60 NCNCRVCAGYFRPKKFCSSSTHNAECEIEGFHCLGPQCTCEKDCRPGQELTKQGCKTC 119  
 Db 61 TCDICRQCKGVFRTRKECSSTNSAECDCPTGFHCLGAGCSMCEQDCKQQLTKGCKDC 120  
 QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
 Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPPADLSPGAS-SVTTP-AP 177  
 QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSLVWKWKPKKPPHIFKQPFKKTGAAQE 235  
 Db 178 AREPGHSPQIISFFLALTSTALLFLLFLLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE 237  
 QY 236 EDACSCRCPOEEGG 250  
 Db 238 EDGCSRCRFPPEEGG 252

RESULT 13  
 US-10-418-242-13  
 Sequence 13, Application US/10418242  
 Publication No. US20040013664A1  
 GENERAL INFORMATION:  
 APPLICANT: Gentz et al.  
 TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
 FILE REFERENCE: PF454P3  
 CURRENT APPLICATION NUMBER: US/10/418,242  
 CURRENT FILING DATE: 2003-04-18  
 PRIOR APPLICATION NUMBER: 60/373,604  
 PRIOR FILING DATE: 2002-04-19  
 PRIOR APPLICATION NUMBER: 09/935,727  
 PRIOR FILING DATE: 2001-08-24  
 PRIOR APPLICATION NUMBER: 60/303,224  
 PRIOR FILING DATE: 2001-07-06  
 PRIOR APPLICATION NUMBER: 60/252,131  
 PRIOR FILING DATE: 2000-11-21  
 PRIOR APPLICATION NUMBER: 60/227,598  
 PRIOR FILING DATE: 2000-08-25  
 PRIOR APPLICATION NUMBER: 09/518,931  
 PRIOR FILING DATE: 2000-03-03  
 PRIOR APPLICATION NUMBER: 60/168,235  
 PRIOR FILING DATE: 1999-12-01  
 PRIOR APPLICATION NUMBER: 60/146,371  
 PRIOR FILING DATE: 1999-08-02  
 PRIOR APPLICATION NUMBER: 60/131,964  
 PRIOR FILING DATE: 1999-04-30  
 PRIOR APPLICATION NUMBER: 60/131,279  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 51

SEQ ID NO 13  
 LENGTH: 255  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-418-242-13

Query Match 55.7%; Score 795; DB 15; Length 255;  
 Best Local Similarity 58.4%; Pred. No. 1e-62;  
 Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;  
 QY 1 MGNVCYNVVIVLLVGVCEKVGAVQNSCDNCPGTF-C-RKYNPVCKSCPSTFSSIGGQP 59  
 Db 1 MGNVCYNIVATLLVLFNFRTRSLQDPCSNCPAGTFCDNRRNQICSPCPNPSFSSAGGQ 60  
 QY 60 NCNCRVCAGYFRPKKFCSSSTHNAECEIEGFHCLGPQCTCEKDCRPGQELTKQGCKTC 119  
 Db 61 TCDICRQCKGVFRTRKECSSTNSAECDCPTGFHCLGAGCSMCEQDCKQQLTKGCKDC 120  
 QY 120 SLGTFNDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
 Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPPADLSPGAS-SVTTP-AP 177  
 QY 180 G---GHSQVLTFLALTS-ALLLALIFITLLFSLVWKWKPKKPPHIFKQPFKKTGAAQE 235  
 Db 178 AREPGHSPQIISFFLALTSTALLFLLFLLRFSVVKRGRKKLLYIFKQPFMRPVQTTQE 237  
 QY 236 EDACSCRCPOEEGG 250  
 Db 238 EDGCSRCRFPPEEGG 252

RESULT 14  
 US-09-739-394-2  
 Sequence 2, Application US/09739394  
 Patent No. US20010014465A1  
 GENERAL INFORMATION:  
 APPLICANT: Ni, Jian  
 Yu, Guo-Liang  
 Gentz, Reiner  
 TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/739,394  
 FILING DATE: 19-Dec-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/253,549  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brookes, A. Anders  
 REGISTRATION NUMBER: 36,373  
 REFERENCE/DOCKET NUMBER: PF254  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-309-8504  
 TELEFAX: 301-309-8512  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 219 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-394-2
Query Match 45.9%; Score 656; DB 9; Length 219;
Best Local Similarity 51.2%; Pred. No. 2.1e-50;
Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;

QY 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNVCYNIVATLLVLNFERTRSLQDPCSNCP-----32
QY 61 CNICRVCAGYFRFKKFCSTHNAECIEGPHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120
Db 33 -----AGVFRTRKECSTSNABECDCCTPGFHLGAGCSMCEQDCKQGOELTKKGCKDCC 85
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db 86 FGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTTP-APA 142
QY 181 ---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKKFPHIFKQPFKKTGAAQEE 236
Db 143 REPGHSPQIIISFFLALTSTALLFLLFLTLRFSVVKGRKKLLYIFKQPFMRPVQTTQEE 202
QY 237 DACSCRCPOEEEG 250
Db 203 DGCSRCFPPEEEGG 216

RESULT 15
US-10-097-330-2
; Sequence 2, Application US/10097330
; Publication No. US20020127651A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT
; FILE REFERENCE: PF254D1C2
; CURRENT APPLICATION NUMBER: US/10/097,330
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/739,394
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/253,549
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: US 08/816,605
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 60/013,474
; PRIOR FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-330-2
Query Match 45.9%; Score 656; DB 13; Length 219;
Best Local Similarity 51.2%; Pred. No. 2.1e-50;
Matches 130; Conservative 27; Mismatches 55; Indels 42; Gaps 6;

QY 1 MGNVCYNVIVVLLVGCCKVAVQNSCDNCPGTFCKRYNPVCKSCPPSTFSSIGGQPN 60
Db 1 MGNVCYNIVATLLVLNFERTRSLQDPCSNCP-----32
QY 61 CNICRVCAGYFRFKKFCSTHNAECIEGPHCLGPQCTRCCKDCRPGQELTKQGCKTCS 120
Db 33 -----AGVFRTRKECSTSNABECDCCTPGFHLGAGCSMCEQDCKQGOELTKKGCKDCC 85
QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPG 180
Db 86 FGTENDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSSADLSPGAS-SVTTP-APA 142
QY 181 ---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKKFPHIFKQPFKKTGAAQEE 236
Db 143 REPGHSPQIIISFFLALTSTALLFLLFLTLRFSVVKGRKKLLYIFKQPFMRPVQTTQEE 202
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QY 237 DACSCRCPOEEEG 250
Db 203 DGCSRCFPPEEEGG 216

RESULT 16
US-10-375-680-55
; Sequence 55, Application US/10375680
; Publication No. US20040009147A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000E
; CURRENT APPLICATION NUMBER: US/10/375,680
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,234
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-375-680-55
Query Match 34.8%; Score 497; DB 15; Length 132;
Best Local Similarity 63.9%; Pred. No. 1.7e-36;
Matches 85; Conservative 13; Mismatches 33; Indels 2; Gaps 2;

QY 28 CDNCQPGTFCR-KYNPVCKSCPPSTFSSIGGQPNICRVCAGYFRFKKFCSTHNAEC 86
Db 1 CSNCPAGTFCDWNRNQCPCPPNSFSSAGGQRTCDICRQCKGVFRTRKECSTNAECD 60
QY 87 CIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCSLGTFNDQNGTGVCRPWTNCSLDGRSV 146
Db 61 CTPGFHCLGAGCSMCEQDCKQGOELTKKGCKDCCFGTFNKQK-RGICRPWTNCSLDGKSV 119
QY 147 LKTGTTEKDVVCG 159
Db 120 LVNGTKERDVVCG 132

RESULT 17
US-10-087-192-939
; Sequence 939, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 939
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-939
Query Match 16.6%; Score 237; DB 12; Length 402;
Best Local Similarity 27.0%; Pred. No. 8.5e-13;
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Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;  
QY 28 CDNCQPGTF-----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVCAGYFRFKKF--CSS 79  
Db 72 CSRCPPGEFVFAVCSRSQDTVCKTCHNSYNEHWNHLSLTCQLCRPCDIVLGFEEVAPCTS 131  
QY 80 THNAECEIEGHC--LGPQCTRCEKD-----CRPGQEL-----TKQCKTCSLGTG- 124  
Db 132 DRKAECRCQPGMCSVYLDNECVHCEERLVLCQPGTEAEVTDVNCVPCPKPGHFQ 191  
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGHSL 184  
Db 192 NTSSPRARCPQPHTRCEIQGLVEAAPTGSYSDTICKNP-----PEPG----- 232  
QY 185 QVLTFLALTSALLLALIFITILLFSLVKWIR-----KKFPHIFKQPFKKTGAAQEEEDAC 239  
Db 233 --AMLLAILLSLVFLFTTVL--ACAWMRHPSLCRKLGLTLKR-----HPEGEESP 281  
QY 240 SCRCPQEE 247  
Db 282 PCPAPRAD 289

RESULT 18  
US-09-826-212-6  
; Sequence 6, Application US/09826212  
; Patent No. US20010021516A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; APPLICANT: Ni, Jian  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1488.128006  
; CURRENT APPLICATION NUMBER: US/09/826,212  
; CURRENT FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 6  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-826-212-6

Query Match 16.6%; Score 237; DB 9; Length 415;  
Best Local Similarity 27.0%; Pred. No. 8.9e-13;  
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;  
QY 28 CDNCQPGTF-----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVCAGYFRFKKF--CSS 79  
Db 59 CSRCPPGEFVFAVCSRSQDTVCKTCHNSYNEHWNHLSLTCQLCRPCDIVLGFEEVAPCTS 118  
QY 80 THNAECEIEGHC--LGPQCTRCEKD-----CRPGQEL-----TKQCKTCSLGTG- 124  
Db 119 DRKAECRCQPGMCSVYLDNECVHCEERLVLCQPGTEAEVTDVNCVPCPKPGHFQ 178  
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGHSL 184  
Db 179 NTSSPRARCPQPHTRCEIQGLVEAAPTGSYSDTICKNP-----PEPG----- 219  
QY 185 QVLTFLALTSALLLALIFITILLFSLVKWIR-----KKFPHIFKQPFKKTGAAQEEEDAC 239  
Db 220 --AMLLAILLSLVFLFTTVL--ACAWMRHPSLCRKLGLTLKR-----HPEGEESP 268  
QY 240 SCRCPQEE 247  
Db 269 PCPAPRAD 276

RESULT 19  
US-09-907-372-20  
; Sequence 20, Application US/09907372  
; Patent No. US20020068242A1

GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti G.  
; APPLICANT: Warren, Bridget A.  
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT  
; FILE REFERENCE: PC-0050 US  
; CURRENT APPLICATION NUMBER: US/09/907,372  
; CURRENT FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PERL Program  
; SEQ ID NO 20  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020068242A1 g600223  
US-09-907-372-20

Query Match 16.6%; Score 237; DB 9; Length 415;  
Best Local Similarity 27.0%; Pred. No. 8.9e-13;  
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;  
QY 28 CDNCQPGTF-----CRKYNPVCKSCPPSTFSSIGGQ-PNCNICRVCAGYFRFKKF--CSS 79  
Db 59 CSRCPPGEFVFAVCSRSQDTVCKTCHNSYNEHWNHLSLTCQLCRPCDIVLGFEEVAPCTS 118  
QY 80 THNAECEIEGHC--LGPQCTRCEKD-----CRPGQEL-----TKQCKTCSLGTG- 124  
Db 119 DRKAECRCQPGMCSVYLDNECVHCEERLVLCQPGTEAEVTDVNCVPCPKPGHFQ 178  
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGHSL 184  
Db 179 NTSSPRARCPQPHTRCEIQGLVEAAPTGSYSDTICKNP-----PEPG----- 219  
QY 185 QVLTFLALTSALLLALIFITILLFSLVKWIR-----KKFPHIFKQPFKKTGAAQEEEDAC 239  
Db 220 --AMLLAILLSLVFLFTTVL--ACAWMRHPSLCRKLGLTLKR-----HPEGEESP 268  
QY 240 SCRCPQEE 247  
Db 269 PCPAPRAD 276

RESULT 20  
US-09-935-727-8  
; Sequence 8, Application US/09935727  
; Patent No. US20020150583A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PF454P2  
; CURRENT APPLICATION NUMBER: US/09/935,727  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/303,224  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/252,131  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/227,598  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: 09/518,931  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/168,235  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 60/146,371  
; PRIOR FILING DATE: 1999-08-02  
; PRIOR APPLICATION NUMBER: 60/131,964  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/131,270  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/124,092  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/121,774  
; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-727-8

Query Match
Best Local Similarity 16.6%; Score 237; DB 9; Length 415;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCQPGTF----CRKYNPVCKSCPPSTFSSIGGQ-PNCNCRVCAGYFRFKKF--CSS 79
Db 59 CSRCPPGEFVFAVCSRSQDTVCKTCHNSYNEHWNHLSTCQLCRPCDIVLGFEVAPCTS 118
QY 80 THNAECECIEGFHC--LGPQCTRCED---CRPGQEL-----TKQCKTCSLGTG- 124
Db 119 DRKAECRCQPGMCSVYLDNECVHCEERLVLCQPGTEAEVTDVNCVPCXPGHFQ 178
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTPEGPGGHSL 184
Db 179 NTSSPRARCQPHTRCEIQGLVEAAPGTSYSDTICKNP-----PEPG----- 219
QY 185 QVTLFLALTSALLALIFITLLFSVLKWR-----KKFPHIFKQPKKTTGAAQEDAC 239
Db 220 --AMLLAILLSVLFLFTTVL--ACAWMRHPSLCRKLGLTLLKR-----HPEGEESP 268
QY 240 SCRCPQEE 247
Db 269 PCPAPRAD 276

RESULT 21
US-09-917-372-20
; Sequence 20, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; CURRENT FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030068619A1 g600223
US-09-917-372-20

Query Match
Best Local Similarity 16.6%; Score 237; DB 10; Length 415;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCQPGTF----CRKYNPVCKSCPPSTFSSIGGQ-PNCNCRVCAGYFRFKKF--CSS 79
Db 59 CSRCPPGEFVFAVCSRSQDTVCKTCHNSYNEHWNHLSTCQLCRPCDIVLGFEVAPCTS 118
QY 80 THNAECECIEGFHC--LGPQCTRCED---CRPGQEL-----TKQCKTCSLGTG- 124
Db 119 DRKAECRCQPGMCSVYLDNECVHCEERLVLCQPGTEAEVTDVNCVPCXPGHFQ 178
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTPEGPGGHSL 184

Db 179 NTSSPRARCQPHTRCEIQGLVEAAPGTSYSDTICKNP-----PEPG----- 219
QY 185 QVTLFLALTSALLALIFITLLFSVLKWR-----KKFPHIFKQPKKTTGAAQEDAC 239
Db 220 --AMLLAILLSVLFLFTTVL--ACAWMRHPSLCRKLGLTLLKR-----HPEGEESP 268
QY 240 SCRCPQEE 247
Db 269 PCPAPRAD 276

RESULT 22
US-10-186-643-6
; Sequence 6, Application US/10186643
; Publication No. US20030118546A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/10/186,643
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-643-6

Query Match
Best Local Similarity 16.6%; Score 237; DB 14; Length 415;
Matches 67; Conservative 33; Mismatches 90; Indels 58; Gaps 12;

QY 28 CDNCQPGTF----CRKYNPVCKSCPPSTFSSIGGQ-PNCNCRVCAGYFRFKKF--CSS 79
Db 59 CSRCPPGEFVFAVCSRSQDTVCKTCHNSYNEHWNHLSTCQLCRPCDIVLGFEVAPCTS 118
QY 80 THNAECECIEGFHC--LGPQCTRCED---CRPGQEL-----TKQCKTCSLGTG- 124
Db 119 DRKAECRCQPGMCSVYLDNECVHCEERLVLCQPGTEAEVTDVNCVPCXPGHFQ 178
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTEKDVVCGPPVVSFSPSTTISVTPEGPGGHSL 184
Db 179 NTSSPRARCQPHTRCEIQGLVEAAPGTSYSDTICKNP-----PEPG----- 219
QY 185 QVTLFLALTSALLALIFITLLFSVLKWR-----KKFPHIFKQPKKTTGAAQEDAC 239
Db 220 --AMLLAILLSVLFLFTTVL--ACAWMRHPSLCRKLGLTLLKR-----HPEGEESP 268
QY 240 SCRCPQEE 247
Db 269 PCPAPRAD 276

RESULT 23
US-10-418-242-8
; Sequence 8, Application US/10418242
; Publication No. US20040013664A1
; GENERAL INFORMATION:
; APPLICANT: Gentz et al.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P3
; CURRENT APPLICATION NUMBER: US/10/418,242
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,604
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/935,727
; PRIOR FILING DATE: 2001-08-24

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; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,279
; PRIOR FILING DATE: 1999-04-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 8
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-418-242-8

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Query Match	16.6%;	Score 237;	DB 15;	Length 415;
Best Local Similarity	27.0%;	Pred. No. 8.9e-13;		
Matches 67;	Conservative 33;	Mismatches 90;	Indels 58;	Gaps 12;

  

QY	28	CDNCQPGTF-----CRKYNPVCKSCPPSTFFSIGGQ-PNCNTRVCAGYFRKKF--CSS 79
		:           :           :           :
Db	59	CSRCPPGEFFAVCSRQDTVCKTCPHNSYNEHWNHLSCTCQLRCPDVLGFEVAPCTS 118
		:           :           :           :
QY	80	THNAECECTEGFHC--LGPQCTRCEKD----CRPGQEL-----TKQGCKTCSLGTG- 124
		:           :           :           :
Db	119	DRKAECRCQPGMCSVYLDNECVHCEEERLVLCQPGTEAEVTDIMDTDVNCVCKPGHFQ 178
		:           :           :           :
QY	125	NDQNGTGVCRPWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTPEGGPGGHS 184
		:           :           :           :
Db	179	NTSSPRARCQPHTRCEIQGLVEAAPGTSYSDTICKNP-----PEPG----- 219
		:           :           :           :
QY	185	QVLTFLFALTSALLLALIFITLLFSVLKWIR-----KKFPHIFKQPFKKTGAAQEEDAC 239
		:           :           :           :
Db	220	--AMLLAILSLVLFLEFTVL--ACAWMRHPSLCRLGLTLLXR-----HPEGEESP 268
		:           :           :           :
QY	240	SCRCPQEE 247
		:           :           :           :
Db	269	PCPAPRAD 276
		:           :           :           :

RESULT 24  
US-09-871-856-15  
; Sequence 15, Application US/09871856  
; Patent No. US20020081720A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; Galibert, Laurent  
; Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immurex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/871,856

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; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15

      15.1%; Score 215; DB 9; Length 625;
      Best Local Similarity 28.6%; Pred. No. 1.3e-10;
      Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY      28 CDNCQPGTF-CRKYNP-----VCKSCPPSTF-SSIGGQPNMCNCRVCAGYFRPKKFCSSSTH 81
Db      48 CSRCEPGKYLSSCKTPTSDSVCLPCGPDYLDLTWNEDKCLLHKVCDAGKALVAVDPGNH 107

QY      82 NA--ECECTEGFH---CLGPQCTRCEKDCRPG-----QELTKQG-CKTCSLGTFTNDQ- 127
Db      108 TAPRRCACTAGYHWNSDC---ECCRRNTECAPGFGAQHPLQLNKDVTCTPCLLGGFFSDVF 164

QY      128 NGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPTTISVTP-EGGPGGHSLOV 186
Db      165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSMTLRRPPEAKAYLPSLIV 217

QY      187 LTLFLALTSALLLALIF-----ITLLFSVLKWKRPKPPHIFKQPKFKTTGAAQEEDA 238
Db      218 LLLFISV--VWVAIIIFGVYRKGGKALTANLWNV-----NDA 254

QY      239 CSCRCPOEEGG 250
Db      255 CSSLSGNKSSG 266

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RESULT 25  
US-09-877-650-15  
; Sequence 15, Application US/09877650  
; Patent No. US20020169117A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; Galibert, Laurent  
; Maraskovsky, Eugene  
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA.

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,363
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-865-363-15

Query Match      15.1%; Score 215; DB 12; Length 625;
Best Local Similarity 28.6%; Pred. No. 1.3e-10;
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKYNP---VCKSCPSTF-SSIGGPNCNICRVAGYFRPKKFCSTH 81
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKLLHKVCDAGKALVAVDPGNH 107

QY 82 NA--EGECIEGFH----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTFTNQ- 127
Db 108 TAPRRCACTAGYHWNSDC---ECCRRNTECAPGFGAQHPLQLNKDTCVCTPLLGFPSDFV 164

QY 128 NGTVGCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186
Db 165 SSTDKCPWTNCTLLGKLEAHQGTTESDVVC-----SSSMTLRRPPKKAQAYLPSLIV 217

QY 187 LTLFLAITSALLLALIF-----ITLLFSVLKWKIRKPPHIFKQPFKKTGAAQEEDA 238
Db 218 LLLFISV--VVVAAILFGVYRKGGKALTANLWNWV-----NDA 254

QY 239 CSCRCPQEEGG 250
Db 255 CSSLSGNKESSG 266

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RESULT 27
US-10-151-071-2
; Sequence 2, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William
; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-151-071-2

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Query Match 15.1%; Score 215; DB 12; Length 625;  
Best Local Similarity 28.6%; Pred. No. 1.3e-10;  
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VCKSCPPSTF-SSIGQPNICRVAGYFRFKKFCSTH 81  
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107

QY 82 NA--ECECIEGFH----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127  
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVF 164

QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186  
Db 165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSMTLRRPPKEAQAYLPSLIV 217

QY 187 LTLFLALTSALLLALIF-----ITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEDA 238  
Db 218 LLLFISV--VVAAIIFGVYRKGKALTANLWNWV-----NDA 254

QY 239 CSCRCPQEEGG 250  
Db 255 CSSLSGNKSSG 266

RESULT 28  
US-09-957-944-4  
; Sequence 4, Application US/09957944  
; Publication No. US2002086312A1  
; GENERAL INFORMATION:  
; APPLICANT: Dougall, William C.  
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS AND ANTAGONISTS OF RECEPTOR ACTIVATION  
; FILE REFERENCE: 3109-A  
; CURRENT APPLICATION NUMBER: US/09/957,944  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/235,157  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 625  
; TYPE: PRT  
; ORGANISM: Mus sp.

Query Match 15.1%; Score 215; DB 12; Length 625;  
Best Local Similarity 28.6%; Pred. No. 1.3e-10;  
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VCKSCPPSTF-SSIGQPNICRVAGYFRFKKFCSTH 81  
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107

QY 82 NA--ECECIEGFH----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127  
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVF 164

QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186  
Db 165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSMTLRRPPKEAQAYLPSLIV 217

QY 187 LTLFLALTSALLLALIF-----ITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEDA 238  
Db 218 LLLFISV--VVAAIIFGVYRKGKALTANLWNWV-----NDA 254

QY 239 CSCRCPQEEGG 250  
Db 255 CSSLSGNKSSG 266

RESULT 29  
US-09-957-944-4

; Sequence 2, Application US/10166232A  
; Publication No. US20030021785A1  
; GENERAL INFORMATION:  
; APPLICANT: DOUGALL, William, C.  
; TITLE OF INVENTION: USE OF RANK ANTAGONISTS TO TREAT CANCER  
; FILE REFERENCE: 3278-A  
; CURRENT APPLICATION NUMBER: US/10/166,232A  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: 60/296,670  
; PRIOR FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 625  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-10-166-232A-2

Query Match 15.1%; Score 215; DB 14; Length 625;  
Best Local Similarity 28.6%; Pred. No. 1.3e-10;  
Matches 72; Conservative 27; Mismatches 91; Indels 62; Gaps 14;

QY 28 CDNCQPGTF-CRKNP-----VCKSCPPSTF-SSIGQPNICRVAGYFRFKKFCSTH 81  
Db 48 CSRCEPGKYLSSKCTPTSDSVCLPCGPDYLDTWNEEDKCLLHKVCDAGKALVAVDPGNH 107

QY 82 NA--ECECIEGFH----CLGPQCTRCCKDCRPG-----QELTKQG-CKTCSLGTENDQ- 127  
Db 108 TAPRRCACTAGYHNSDC---ECCRRNTECAPGFGAHPQLQNKDVTCTPCLLGFSDVF 164

QY 128 NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTP-EGGPGGHSLOV 186  
Db 165 SSTDKCKPWTNCTLLGKLEAHQGTTESDVVC-----SSMTLRRPPKEAQAYLPSLIV 217

QY 187 LTLFLALTSALLLALIF-----ITLLFSVLKWKIRKFPFHIFKQPFKKTGAAQEEDA 238  
Db 218 LLLFISV--VVAAIIFGVYRKGKALTANLWNWV-----NDA 254

QY 239 CSCRCPQEEGG 250  
Db 255 CSSLSGNKSSG 266

RESULT 30  
US-10-405-878-15  
; Sequence 15, Application US/10405878  
; Publication No. US20030175840A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; Galibert, Laurent  
; Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/405,878  
; FILING DATE: 01-Apr-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,139  
; FILING DATE: 22 DECEMBER 1997

Query Match 15.0%; Score 214.5; DB 9; Length 277;  
Best Local Similarity 25.7%; Pred. NO. 5.6e-11;  
Matches 67; Conservative 39; Mismatches 106; Indels 49; Gaps 11;

100

Patent No. US20020127637A1  
GENERAL INFORMATION:  
APPLICANT: NI, JIAN  
MOORE, PAUL  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR  
RECEPTOR-LIKE PROTEIN 8  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/768,779A  
FILING DATE: 25-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/086,582  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: KENLEY K. HOOVER  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PF368PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 615 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-768-779A-2

Query Match 14.7%; Score 209.5; DB 9; Length 615;  
Best Local Similarity 30.4%; Pred. No. 3.9e-10;  
Matches 62; Conservative 25; Mismatches 70; Indels 47; Gaps 11;  
QY 28 CDNCQPGTFCRK-----YNPVCKSCPPSTF-SSIGGQPNICRVC-----AGYF 71  
Db 46 CNKCEPGKYMSSKCTTSDSVCLPCGPDYLDVDSWNEEDKLLHKVCDTGKALVAVAG-- 103  
QY 72 RPKKFCSTHNAECEICIEGFH---CLGPQCTRCCKDCRPG-----QELTKQG-CKTCS 120  
Db 104 -----NSTTPRRCACTAGYHWSQDC---ECCRRNTECAPGLGAHQHPLQNKDITVCKPCL 154  
QY 121 LGTFNDQ-NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 155 AGYFSDAFSSTDKCRPWTNCTFLGKRVEHHGTEKSDVVCSSSLPARKPPNEPHVYLP-- 212  
QY 180 GGHSLQVLTFLALTSALLLALIF 203  
Db 213 ----LIILLFASV--ALVAAIIF 230

RESULT 34  
US-10-291-480-2  
Sequence 2, Application US/10291480  
Publication No. US20030100069A1  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Moore, Paul  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8  
FILE REFERENCE: PF368C1d1  
CURRENT APPLICATION NUMBER: US/10/291,480

CURRENT FILING DATE: 2002-11-12  
PRIOR APPLICATION NUMBER: 09/768,779  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 09/086,582  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/048,020  
PRIOR FILING DATE: 1997-05-29  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 615  
TYPE: PRT  
ORGANISM: human  
US-10-291-480-2  
Query Match 14.7%; Score 209.5; DB 14; Length 615;  
Best Local Similarity 30.4%; Pred. No. 3.9e-10;  
Matches 62; Conservative 25; Mismatches 70; Indels 47; Gaps 11;  
QY 28 CDNCQPGTFCRK-----YNPVCKSCPPSTF-SSIGGQPNICRVC-----AGYF 71  
Db 46 CNKCEPGKYMSSKCTTSDSVCLPCGPDYLDVDSWNEEDKLLHKVCDTGKALVAVAG-- 103  
QY 72 RPKKFCSTHNAECEICIEGFH---CLGPQCTRCCKDCRPG-----QELTKQG-CKTCS 120  
Db 104 -----NSTTPRRCACTAGYHWSQDC---ECCRRNTECAPGLGAHQHPLQNKDITVCKPCL 154  
QY 121 LGTFNDQ-NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGP 179  
Db 155 AGYFSDAFSSTDKCRPWTNCTFLGKRVEHHGTEKSDVVCSSSLPARKPPNEPHVYLP-- 212  
QY 180 GGHSLQVLTFLALTSALLLALIF 203  
Db 213 ----LIILLFASV--ALVAAIIF 230

RESULT 35  
US-09-826-212-10  
Sequence 10, Application US/09826212  
Patent No. US20010021516A1  
GENERAL INFORMATION:  
APPLICANT: Wei, Ying-Fei  
APPLICANT: Gentz, Reiner  
APPLICANT: Ruben, Steven  
APPLICANT: Ni, Jian  
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
FILE REFERENCE: 1488.1280006  
CURRENT APPLICATION NUMBER: US/09/826,212  
CURRENT FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 277  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-826-212-10

Query Match 14.6%; Score 208.5; DB 9; Length 277;  
Best Local Similarity 25.7%; Pred. No. 1.9e-10;  
Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;  
QY 18 CEKVGAVQNS--CDNCQPG-----TFCKKYNPV-CKSCPPSTF-SSIGGQPNICRVCAG 69  
Db 26 CREKQYLINSQCCLCPGQKLVSDCTEFTETECPLCGESEFLDTWNRHCHQHKYCDP 85  
QY 70 Y--FRPKKFCSTHNAECEICIEGFHCLGPQCTRC--EKDCRPG-----QELTKQGCKT 118  
Db 86 NLGLRVQKGTSETDTICTCEEGWHCTSEACESCVLHRSVCSGFGVKQIATGVSDTICEP 145  
QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177  
Db 146 CPVGFFSNVSSAFCKEHPWTSCETKDLVVQQAGTKNTDVCVGPQ----- 189

QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKFFPHFKQPFK-----K 228  
Db 190 -DRLRALVVIPIIFGILFAILLVLVFIK--KVAKKPTNKAPHPKQEPQEIFPDDLPGS 245  
QY 229 TTGAQAEEDACSCRCPOEEG 249  
Db 246 NTAAPVQETLHGCPVTQEDG 266

RESULT 36  
US-09-768-779A-4  
; Sequence 4, Application US/09768779A  
; Patent No. US20020127637A1  
; GENERAL INFORMATION:  
; APPLICANT: NI, JIAN  
; MOORE, PAUL  
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR  
; RECEPTOR-LIKE PROTEIN 8  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/768,779A  
; FILING DATE: 25-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/086,582  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KENLEY K. HOOVER  
; REGISTRATION NUMBER: 40,302  
; REFERENCE/DOCKET NUMBER: PF368PP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-768-779A-4

Query Match 14.6%; Score 208.5; DB 9; Length 277;  
Best Local Similarity 25.7%; Pred. No. 1.9e-10;  
Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;  
QY 18 CEKVGAVQNS--CDNCQPG---TFCKKNPV-CKSCPPSTF-SSIGGQPNICRVACG 69  
Db 26 CREKQYLINSQCCSLCQPGQKLVSDCTETETECPCGESEFLDTWNRETHCHQHKYCDP 85  
QY 70 Y--FRFKFCSSTHNAECIEGFHCLGPQCTRC--EKDCRPG-----QELTKQGCKT 118  
Db 86 NLGLRVQKGTSETDICTCEEGHCTSEACESCVLHRSCTSPGFGVKQIATGVSDTICEP 145  
QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177  
Db 146 CPVGFSSNVSSAFKCHPWTSCETKDLVQQAGTKNTDVVCGPQ-----189  
QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKFFPHFKQPFK-----K 228

Db 190 -DRLRALVVIPIIFGILFAILLVLVFIK--KVAKKPTNKAPHPKQEPQEIFPDDLPGS 245  
QY 229 TTGAQAEEDACSCRCPOEEG 249  
Db 246 NTAAPVQETLHGCPVTQEDG 266  
RESULT 37  
US-09-935-727-12  
; Sequence 12, Application US/09935727  
; Patent No. US20020150583A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PF454P2  
; CURRENT APPLICATION NUMBER: US/09/935,727  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/303,224  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/252,131  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/227,598  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: 09/518,931  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/168,235  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 60/146,371  
; PRIOR FILING DATE: 1999-08-02  
; PRIOR APPLICATION NUMBER: 60/131,964  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/131,270  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/124,092  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/121,774  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: 09/006,352  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: 60/035,496  
; PRIOR FILING DATE: 1997-01-14  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-727-12

Query Match 14.6%; Score 208.5; DB 9; Length 277;  
Best Local Similarity 25.7%; Pred. No. 1.9e-10;  
Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;  
QY 18 CEKVGAVQNS--CDNCQPG---TFCKKNPV-CKSCPPSTF-SSIGGQPNICRVACG 69  
Db 26 CREKQYLINSQCCSLCQPGQKLVSDCTETETECPCGESEFLDTWNRETHCHQHKYCDP 85  
QY 70 Y--FRFKFCSSTHNAECIEGFHCLGPQCTRC--EKDCRPG-----QELTKQGCKT 118  
Db 86 NLGLRVQKGTSETDICTCEEGHCTSEACESCVLHRSCTSPGFGVKQIATGVSDTICEP 145  
QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177  
Db 146 CPVGFSSNVSSAFKCHPWTSCETKDLVQQAGTKNTDVVCGPQ-----189  
QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKFFPHFKQPFK-----K 228  
Db 190 -DRLRALVVIPIIFGILFAILLVLVFIK--KVAKKPTNKAPHPKQEPQEIFPDDLPGS 245  
QY 229 TTGAQAEEDACSCRCPOEEG 249  
Db 246 NTAAPVQETLHGCPVTQEDG 266

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RESULT 38
US-10-328-953-323
; Sequence 323, Application US/10328953
; Publication No. US20040071656A1
; GENERAL INFORMATION:
; APPLICANT: Wieland, Felix
; APPLICANT: Hartl, Franz-Ulrich
; TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
; FILE REFERENCE: 11390/46101
; CURRENT FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2001-12-26
; PRIOR FILING DATE: 2001-12-26
; PRIOR FILING DATE: 2001-12-28
; PRIOR FILING DATE: 2002-04-12
; PRIOR FILING DATE: 2002-07-29
; PRIOR FILING DATE: 2002-09-28
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 323
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-328-953-323

Query Match      14.6%; Score 208.5; DB 12; Length 277;
Best Local Similarity 25.7%; Pred. No. 1.9e-10;
Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;

QY 18 CEKVGAVQNS--CDNCQPG-----TFCRKYNPV-CKSCPPSTF-SSIGGQPNICRVCA 69
Db 26 CREKQYLINSQCCLQPGQKLVSDCTETETECCLPGGESEFLDTWNRTHCHQHKYCDP 85
QY 70 Y--FRFKKFCSTHNAECEIEGFHCLGPQCTRC--EKDCRPG-----QELTKQGCKT 118
Db 86 NLGLRVQKGTSETDTICTCEEGWHCTSEACSVLHRSCTSPGFGVKQIATGVSDTICEP 145
QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
Db 146 CPVGFSSNVSSAFKCHPWTSCETKDLVVQAGTKNTDVVCGPQ-----189
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; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 323
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-328-953-323

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RESULT 39
US-10-291-480-4
; Sequence 4, Application US/10291480
; Publication No. US20030100069A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: PF368C1D1
; CURRENT FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 1998-05-28
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 24

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 277
; TYPE: PRT
; ORGANISM: human
US-10-291-480-4

Query Match      14.6%; Score 208.5; DB 14; Length 277;
Best Local Similarity 25.7%; Pred. No. 1.9e-10;
Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;

QY 18 CEKVGAVQNS--CDNCQPG-----TFCRKYNPV-CKSCPPSTF-SSIGGQPNICRVCA 69
Db 26 CREKQYLINSQCCLQPGQKLVSDCTETETECCLPGGESEFLDTWNRTHCHQHKYCDP 85
QY 70 Y--FRFKKFCSTHNAECEIEGFHCLGPQCTRC--EKDCRPG-----QELTKQGCKT 118
Db 86 NLGLRVQKGTSETDTICTCEEGWHCTSEACSVLHRSCTSPGFGVKQIATGVSDTICEP 145
QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
Db 146 CPVGFSSNVSSAFKCHPWTSCETKDLVVQAGTKNTDVVCGPQ-----189
QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKFFHFKQPFK-----K 228
Db 190 -DRLRALVVIPIIFGILFALLVLVFIK---KVAKKPTNKAPHKQEPQEIFPDDLP 245
QY 229 TTGAQAEEDACSCRCPOEEEG 249
Db 246 NTAAPVQETLHGCPVTQEDG 266

RESULT 40
US-10-186-643-10
; Sequence 10, Application US/10186643
; Publication No. US20030118546A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT FILING DATE: 2002-07-02
; PRIOR FILING DATE: 2002-07-02
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-643-10

Query Match      14.6%; Score 208.5; DB 14; Length 277;
Best Local Similarity 25.7%; Pred. No. 1.9e-10;
Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;

QY 18 CEKVGAVQNS--CDNCQPG-----TFCRKYNPV-CKSCPPSTF-SSIGGQPNICRVCA 69
Db 26 CREKQYLINSQCCLQPGQKLVSDCTETETECCLPGGESEFLDTWNRTHCHQHKYCDP 85
QY 70 Y--FRFKKFCSTHNAECEIEGFHCLGPQCTRC--EKDCRPG-----QELTKQGCKT 118
Db 86 NLGLRVQKGTSETDTICTCEEGWHCTSEACSVLHRSCTSPGFGVKQIATGVSDTICEP 145
QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
Db 146 CPVGFSSNVSSAFKCHPWTSCETKDLVVQAGTKNTDVVCGPQ-----189
QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKFFHFKQPFK-----K 228
Db 190 -DRLRALVVIPIIFGILFALLVLVFIK---KVAKKPTNKAPHKQEPQEIFPDDLP 245
QY 229 TTGAQAEEDACSCRCPOEEEG 249
Db 246 NTAAPVQETLHGCPVTQEDG 266

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Db 190 -DRLRALVVIPIIFGILFAILLVLVFIK---KVAKKPTNKAPHPKQEPQEIINFPPDDLPGS 245  
QY 229 TTGAAQBEEDACSRCPQEEEG 249  
Db 246 NTAAPVQETLHGCQPVTOEDG 266

Search completed: May 5, 2004, 14:53:53  
Job time : 96.6849 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:41 ; Search time 30.6849 Seconds  
(without alignments)  
802.512 Million cell updates/sec

Title: US-10-067-122B-2

Perfect score: 1428

Sequence: 1 MGNVCYVNVVIVLLVGEK.....DACSCRCPEEGGGGYEL 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Match	Length	DB	ID	Description
1	1428	100.0	256	2	B32393	T-cell antigen 4-1
2	795	55.7	255	2	I38426	lymphocyte activat
3	208.5	14.6	277	2	A60771	B-cell activation
4	202.5	14.2	277	2	I37552	OX40 homolog - hum
5	202	14.1	435	2	I54182	tumor necrosis fac
6	197	13.8	461	1	A35356	tumor necrosis fac
7	186.5	13.1	305	2	A46476	B cell-associated
8	185	13.0	474	2	B38634	tumor necrosis fac
9	182	12.7	459	2	I48854	gene murine tumour
10	173	12.1	651	2	JC7705	death receptor-6 -
11	170.5	11.9	271	2	S12783	OX40 antigen precu
12	169.5	11.9	250	1	A49053	CD27 antigen precu
13	166.5	11.7	260	1	A46517	CD27 antigen precu
14	158	11.1	272	2	I48700	gene OX40 protein
15	142	9.9	349	2	D72175	G2R protein - vari
16	140.5	9.8	325	2	B43692	T2 protein - rabbi
17	139.5	9.8	416	1	JN0006	nerve growth facto
18	138	9.7	348	2	T28623	hypothetical prote
19	138	9.7	349	2	D36858	gene G4R protein -
20	138	9.7	3106	1	S53868	laminin alpha-2 ch
21	135.5	9.5	713	2	A35502	major surface-labe
22	135	9.5	427	1	GQHUN	nerve growth facto
23	135	9.5	656	2	JC2005	integrin beta-5 ch
24	135	9.5	799	2	A38308	integrin beta-5 ch
25	133	9.3	425	1	A26431	nerve growth facto
26	130.5	9.1	326	1	GQVZML	T2 protein - myxom
27	129	9.0	1797	2	A55677	laminin beta-2 cha
28	129	9.0	3635	2	T10053	laminin alpha 5 ch
29	127	8.9	461	1	QORTT1	tumor necrosis fac

30	126	8.8	3707	2	S18252	heparan sulfate pr
31	125.5	8.8	3084	1	MMMSA	laminin alpha-1 ch
32	125	8.8	4135	2	T42629	tenascin-X - bovin
33	124.5	8.7	1786	1	MMHUB1	laminin beta-1 cha
34	124	8.7	899	2	G02428	subtilisin-like pr
35	124	8.7	915	2	JC6148	subtilisin-like pr
36	123.5	8.6	3075	2	S14458	laminin alpha-1 ch
37	123.5	8.6	3712	2	S18253	laminin alpha-1 ch
38	122.5	8.6	1609	1	MMHUB2	laminin gamma-1 ch
39	122.5	8.6	2824	2	T22759	hypothetical prote
40	122.5	8.6	3672	2	T23433	hypothetical prote
41	122.5	8.6	3704	2	T37316	probable laminin a
42	120.5	8.4	1607	1	MMMSB2	laminin gamma-1 ch
43	120.5	8.4	1786	1	MMMSB1	laminin beta-1 cha
44	120.5	8.4	2823	2	T23064	hypothetical prote
45	120.5	8.4	2823	2	F87908	protein T22A3.8 [i

ALIGNMENTS

RESULT 1

B32393  
T-cell antigen 4-1BB precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C:Accession: B32393; I48879  
R;Kwon, B.S.; Weissman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A;Title: cDNA sequence of two inducible T-cell genes.  
A;Reference number: A32393; MUID:89184547; PMID:2784565  
A;Accession: B32393  
A;Molecule type: mRNA  
A;Residues: 1-256 <KWO>  
A;Cross-references: GS:J04492; NID:G201121; PIDN:AAA40167.1; PID:G201122  
R;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994  
A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.  
A;Reference number: I48879; MUID:94179805; PMID:8133039  
A;Accession: I48879  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-256 <RES>  
A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178  
A;Genetics:  
A;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: transmembrane protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 100.0%; Score 1428; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 4.8e-98;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGNVCYVNVVIVLLVGEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN	60
Db	1	MGNVCYVNVVIVLLVGEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPN	60
QY	61	CNCRVCAGYFRFKKFCSSSTHNAECIEGHCILGPQCTRCCKDCRPGQELTKQCKTCS	120
Db	61	CNCRVCAGYFRFKKFCSSSTHNAECIEGHCILGPQCTRCCKDCRPGQELTKQCKTCS	120
QY	121	LGTENDQGTGVCRPWTNCSLDGRSVLKTGTTEKDVWCGPPVVSFSPSTTISVTPGGPG	180
Db	121	LGTENDQGTGVCRPWTNCSLDGRSVLKTGTTEKDVWCGPPVVSFSPSTTISVTPGGPG	180
QY	181	GHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKFFPHFKQPFKKTGAQEEEDACS	240
Db	181	GHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKFFPHFKQPFKKTGAQEEEDACS	240
QY	241	CRCPEEGGGGYEL 256	

Db 241 CRCPQEEGGGGYEL 256

## RESULT 2

I38426

lymphocyte activation-induced receptor ILA precursor - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000

C;Accession: I38426; J07052

R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R

Eur. J. Immunol. 24, 2219-2227, 1994

A;Title: Molecular and biological characterization of human 4-1BB and its ligand.

A;Reference number: I38426; MUID:94374434; PMID:8088337

A;Accession: I38426

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-255 <RES>

A;Cross-references: EMBL:U03397; NID:G571320; PIDN:AAAS3133.1; PID:G571321

R;Schwarz, H.; Tuckwell, J.; Lotz, M.

Gene 134, 295-298, 1993

A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne

A;Reference number: J07052; MUID:94085794; PMID:8262389

A;Accession: J07052

A;Molecule type: mRNA

A;Residues: 1-106, 'R', 108-255 <SCH>

C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro

C;Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix

C;Superfamily: CD27 antigen; NGF receptor repeat homology

C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>

F;187-213/Domain: transmembrane #status predicted <TM>

F;138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict

F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

## Query Match

Best Local Similarity 55.7%; Score 795; DB 2; Length 255;

Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNVCYNVIVLLVGGCKVAVQNSCDNCQPGTFC-RKYNPVCKSCPPSTFSSIGGQP 59

Db 1 MGNVCYNIVATLLVLFNFRTRSLQDPCSNCPAGTFCDDNNRNIQICPCPPNSFSSAGGQR 60

QY 60 NCNICRVACGYFRFKFCSSSTHNAECEIEGFHCLGPOCTRCERKCPQELTKQCKTC 119

Db 61 TCDICRQCKGVFRTRKECSSTNAECDTPGFHCLGAGCSMCEQCKQGGELTKKCKDC 120

QY 120 SLGTENDQGTGVCPRWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGP 179

Db 121 CFGTFNDQK-RGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGAS-SVTPP-AP 177

QY 180 G---GHSLQVLTFLALTS-ALLLALIFITLLFSLVKWIRKFPFHIFKQPFKTTGAAQE 235

Db 178 AREPGHSPQIIISFFLALTSTALLFLFLFTLRFVSVKRKKLLYIFKQPFMRVQTQOE 237

QY 236 EDACSCRCPQEEEGG 250

Db 238 EDGCSRCFPPEEEEGG 252

RESULT 3

A60771

B-cell activation protein CD40 precursor - human

N;Alternate names: B-cell surface antigen Bp50

C;Species: Homo sapiens (man)

C;Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000

R;Stamenkovic, I.; Clark, E.A.; Seed, B.

EMBO J. 8, 1403-1410, 1989

A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor

A;Reference number: S04460; MUID:89356608; PMID:2475341

A;Accession: S04460

A;Molecule type: mRNA

A;Residues: 1-277 <STA>

A;Cross-references: EMBL:X60592; NID:G29850; PIDN:CAA43045.1; PID:G29851

R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.

J. Immunol. 142, 562-567, 1989

A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like

A;Reference number: A60771; MUID:8903941; PMID:2463309

A;Accession: A60771

A;Molecule type: protein

A;Residues: 21-50 <BRA>

A;Experimental source: Burkitt lymphoma cell line Raji

C;Genetics:

A;Gene: GDB:CD40

A;Cross-references: GDB:215268; OMIM:109535

A;Map position: 20q12-20q13.2

C;Superfamily: CD27 antigen; NGF receptor repeat homology

C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>

F;21-193/Domain: extracellular #status predicted <EXT>

F;194-215/Domain: transmembrane #status predicted <TM>

F;216-277/Domain: intracellular #status predicted <CYT>

F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

## Query Match

Best Local Similarity 14.6%; Score 208.5; DB 2; Length 277;

Matches 67; Conservative 37; Mismatches 108; Indels 49; Gaps 11;

QY 18 CEKVGAVQNS--CDNCQPG----TFCRKYNPV-CKSCPPSTF-SSIGGQPNICRVACG 69

Db 26 CREKQYLINSQCCLQCGQKLVSDCTETETETECPLCGESEFLDTWNPETHCHQHKYCDP 85

QY 70 Y--FRFKFCSSSTHNAECEIEGFHCLGPOCTRC--EKDCRPG-----QELTKQCKT 118

Db 86 NLGLRVQCKGTSETDICTCEEGWHCTSEACESCVLHRSCTSPGFGVKQIATGVSDTICEP 145

QY 119 CSLGTF-NDONGTGVCPRWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177

Db 146 CPVGFSSNVSSAFKCHPWTSCETKDLVVQAGTNKTDVVCQPQ----- 189

QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKFPFHIFKQPFK-----K 228

Db 190 -DLRLALVVPIIFGILFAILLVLVFIK---KVAKPTNKAPHKQEPQEPFDDILPGS 245

QY 229 TTGAAQEEEDACSCRCPOEEEG 249

Db 246 NTAAPVQETLHGCPVTQEDG 266

## RESULT 4

I37552

OX40 homolog - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000

C;Accession: I37552

R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Fonats

Eur. J. Immunol. 24, 677-683, 1994

A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment of

A;Reference number: I37552; MUID:94170844; PMID:7510240

A;Accession: I37552

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-277 <RES>

A;Cross-references: EMBL:X75962; NID:G472957; PIDN:CAA53576.1; PID:G472958

C;Superfamily: CD27 antigen; NGF receptor repeat homology

## Query Match

Best Local Similarity 14.2%; Score 202.5; DB 2; Length 277;

Matches 64; Conservative 35; Mismatches 94; Indels 59; Gaps 12;

QY

Db

28

43



Query Match 13.8%; Score 197; DB 1; Length 461;  
Best Local Similarity 26.3%; Pred. No. 2.4e-07;  
Matches 72; Conservative 33; Mismatches 99; Indels 70; Gaps 15;

QY 25 QNSCDNCQPG-----TFCRK-YNPVCKSCPPSTFSSI-GGQPNIC-RVCAGYFRFKFC 77  
Db 51 QMCCSKCSPGQHAQVCTKTSITVDCSDSTVQLWNWPECLSCGSRCSDDQVETQAC 110  
QY 78 SSTHNAECEIEGPHC-LGPQ--CTRCE--KDCRPGQELTKQG-----CKTCSLGTG- 124  
Db 111 TREQNRICTRPGWYCALSKQEGCRLCAPLRKCRPGFGVARGTETSDVVCKPCAPGTFS 170  
QY 125 NDQNGTGVCRPWTNCSLDGRSVLTKGTTEKDVVC----- 158  
Db 171 NTTSSTDICRPHQICNV---VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQH 226  
QY 159 --GPPVVSFSPSTI-----SVTPEGPGGSHSLQVLTFLALTSALLLALIFITLLFSV 210  
Db 227 TOPTPEPSTAPSTSFLLPMGSPPAEGSTGDFALPV-GLIVGVTALGLLIGVWNCV--I 283  
QY 211 LKWIRK-----KFPHFIFKQPFKKTGTGAQE 235  
Db 284 MTQVKKKPLCLQREAKVPHLPADKARGTQGPQQ 317

RESULT 7  
A46476  
B cell-associated surface molecule CD40, long splice form - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C;Accession: A46476; MUID:92105763; PMID:1370315  
R;Torres, R.M.; Clark, E.A.  
J. Immunol. 148, 620-626, 1992  
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine A46476  
A;Reference number: A46476; MUID:92105763; PMID:1370315  
A;Accession: A46476  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-305 <TOR>  
A;Cross-references: GB:M83312; NID:g15533058  
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:75207)  
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992  
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A;Reference number: A46515; MUID:93094586; PMID:1281194  
A;Accession: A46515  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-287, 'LV' <GRI>  
A;Cross-references: GB:M83312; NID:g15533058; PIDN:AAB08705.1; PID:g15533059; GB:M94126; N  
A;Experimental source: BALB/c, liver  
A;Note: sequence extracted from NCBI backbone (NCBI:120357)  
C;Comment: For an alternative splice form, see PIR:A46515.  
C;Comment: For an alternative splice form, see PIR:A46476.  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: alternative splicing; transmembrane protein  
F;105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 13.1%; Score 186.5; DB 2; Length 305;  
Best Local Similarity 25.1%; Pred. No. 1e-06;  
Matches 61; Conservative 34; Mismatches 87; Indels 61; Gaps 11;

QY 28 CDNCQPGTFCRKY-----NPVCKSCPPSTFSSIGGP-NCNICRVAGY--FRFKFCSS 79  
Db 38 CDLCQPGSLTSHCTALEKTOCHPCDSEFSQAQWNRIRCHQHRHCEPNQGLRVKKEGTA 97  
QY 80 THNAECEIEGFHCLGPQCTRCEK--DCRPG-----QELTKQGCKTCSLGTNDQNGT 130  
Db 98 ESDTVCTCKEGQHTSKDCEACAQHTCIPGFGVMEMATETTTDVTCHPCPVGFFSNQSSL 157  
QY 131 -GVCRPWTNCSLDGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGGSHLQVLT 189

Db 158 FEKYPWTSCEDKNLEVLQKGTQTNVIC-----L 188  
QY 190 FLALTSALLLALI--FITLFSVLKWKIRKFFHIFKQP--FKTTGAAQEEADACSCRCPPQ 245  
Db 189 KSRMRALLVIPVVMGILITIFGVLYIKK-----VVKPKDNEMLPPAARRQD-----PQ 238  
QY 246 EEE 248  
Db 239 EME 241

RESULT 8  
B38634  
tumor necrosis factor receptor type 2 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 27-Oct-2003  
C;Accession: B38634; A40254; S54816  
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.  
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor re  
A;Reference number: A38634; MUID:91187885; PMID:1849278  
A;Accession: B38634  
A;Molecule type: mRNA  
A;Residues: 1-474 <LEW>  
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for t  
A;Reference number: A40254; MUID:91246168; PMID:1645445  
A;Accession: A40254  
A;Molecule type: mRNA  
A;Residues: 1-474 <GOO>  
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R;Kisnerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.  
submitted to the EMBL Data Library, May 1995  
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.  
A;Reference number: S54816  
A;Accession: S54816  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-22 <KIS>  
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044  
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog  
C;Keywords: cytokine receptor; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F;40-77/Domain: NGF receptor repeat homology <NG1>  
F;79-120/Domain: NGF receptor repeat homology <NG2>  
F;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 13.0%; Score 185; DB 2; Length 474;  
Best Local Similarity 26.0%; Pred. No. 1.9e-06;  
Matches 75; Conservative 26; Mismatches 107; Indels 80; Gaps 15;

QY 25 QNSCDNCQPGT----FCRK-YNPVCKSCPPSTFSSIGGPNCNICRVAGYFRFK----K 75  
Db 52 QMCCAKCPGQYVVKHFCNKTSDTVACDEASMYTQVWQ--FRTCLSCSSSCTTQDQVEIR 109  
QY 76 FCSSTHNAECEIEGFHCL-----GPQCTRCEKDCRPGQELTKQG-----CKTCSL 121  
Db 110 ACTKQNRVCAACEAGRYCALKTHSGSCRCQMLSK-CGPGFGVASSRAPNGNVLCACAP 168  
QY 122 GTFND-QNGTGVCRPWTNCSLDGRSVLTKGTTEKDVVCGP--PVVSFSPSTTISVTP--- 175  
Db 169 GTFSDTSSSTDVCRPHRCSI---LAIPGNASTDAVCAPESPTLSAIPRTLYVSPEPT 224  
QY 176 -----EGGP-----GGHSLQVLTFLALTSALLLALIFITLL 207  
Db 225 RSQPLDQEPGPGSQTPSILTSLSGTPIEQSTKGGISLPI-GLIVGYS---LGLMLGLV 280  
QY 208 FSVLKWIRKFFHIFKQPFKKTGTGAQEEADACSCRCPOEEGGGGYE 255

Db 281 NCILVQRKKP-----SCLQRDAKVPHVPDEKSDQAVGLE 316

RESULT 9  
I48854  
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 27-Oct-2003  
C;Accession: I48854  
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
Mamm. Genome 5, 726-727, 1994  
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
A;Reference number: I48854; MUID:95178848; PMID:7873884  
A;Accession: I48854  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-459 <RES>  
A;Cross-references: EMBL:X76401; NID:G433830; PIDN:CAA53981.1; PID:G433831  
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog  
F;151-188/Domain: NGF receptor repeat homolog <NGF>

Query Match 12.7%; Score 182; DB 2; Length 459;  
Best Local Similarity 26.6%; Pred. No. 3.1e-06;  
Matches 76; Conservative 25; Mismatches 109; Indels 76; Gaps 15;

QY 25 QNSCDNCQPGT----PCRK-YNPVCKSCPPSTFFSIGGQ-PNCNIC-RVCAGYFRFKKFC 77  
Db 37 QMCCAKCPPGQYVHFCNKTSDTVCADCEASMYQVMNQFRTCLSCSSCSTDQVETRAC 96  
QY 78 SSTHNAECEIEGPHCL-----GPQTRCEKDCRPGQELTKQG-----CKTCSLGT 123  
Db 97 TKQQNRVCAACEAGRYCALKTHSGSCRCQMLSK-CGPGFGVASSRAPNGNVLCACAPGT 155  
QY 124 FND-QNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP--PVVSFSPSTTISVTP----- 175  
Db 156 FSDTSTSDVCRPHRCSI-----LAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRS 211  
QY 176 -----EGGP-----GGHSLQVLTFLALTSALLLALIFITLLFS 209  
Db 212 QPLDQEPGPSQTPSILTSLSGSTPIIEQSTKGGISLPI-GLIVGVS---LGLMLGLVNC 267  
QY 210 VLKWKIRKFPHFIFKQPFKKTGTGAQAEEDACSCRCPOEEGGGGYE 255  
Db 268 FILVQRKKP-----SCLQRDAKVPHVPDEKSDQAVGLE 301

RESULT 10  
JC7705  
death receptor-6 - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 07-Jul-2003  
C;Accession: JC7705  
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.  
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001  
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.  
A;Reference number: JC7705; MUID:21308433; PMID:11414698  
A;Accession: JC7705  
A;Molecule type: mRNA  
A;Residues: 1-651 <BRI>  
A;Cross-references: GB:AF349908  
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF receptor superfamily, a cell death and/or survival signaling cascade.  
C;Genetics:  
A;Gene: dr-6  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homolog  
C;Keywords: ovary  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>  
F;332-350/Domain: transmembrane #status predicted <TM>  
F;410-475/Domain: death domain #status predicted <DED>  
F;551-651/Region: conserved cytoplasmic #status predicted

Query Match 12.1%; Score 173; DB 2; Length 651;

Best Local Similarity 30.0%; Pred. No. 1.9e-05;  
Matches 48; Conservative 22; Mismatches 72; Indels 18; Gaps 7;

QY 28 CDNCPQGTFCRKYNP-----VCKSCPSTFSS-IGQPNCNICR-VCAGYFRFKKCSST 80  
Db 52 CDKCPAGTYVSKHCTKSTLRECSPCDGTFTKHENGIERCHPCRPCELPMEIKTHCTAL 111  
QY 81 HNAECEIEGFHCLGFPQCTRCEKDCRPGQELTKQG-----CKTCSLGTEND-QNGTGV 132  
Db 112 TDRECTCLSGTFOINDTCVPYTV-CPVGGVGRKKGTETEDVRCKPCLRGTGTFSDVPSSVMK 170  
QY 133 CRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTIS 172  
Db 171 CKTYTDCFGKMMVVVXPGTKESDNVCKSP--ASLENTSLT 208

RESULT 11  
S12783  
OX40 antigen precursor - rat  
N;Alternate names: nerve growth factor receptor homolog  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C;Accession: S12783; S08036  
R;Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes  
A;Reference number: S12783; MUID:90214614; PMID:2157591  
A;Accession: S12783  
A;Molecule type: mRNA  
A;Residues: 1-271 <VAL>  
A;Cross-references: EMBL:X17037; NID:G57830; PIDN:CAA34897.1; PID:G57831  
C;Superfamily: CD27 antigen; NGF receptor repeat homolog  
C;Keywords: growth factor receptor; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-271/Product: OX40 antigen #status predicted <MAT>  
F;211-235/Domain: transmembrane #status predicted <TM>

Query Match 11.9%; Score 170.5; DB 2; Length 271;  
Best Local Similarity 24.6%; Pred. No. 1.4e-05;  
Matches 59; Conservative 19; Mismatches 83; Indels 79; Gaps 10;

QY 14 LLVGE-----KVGAVQNS-----CDNCQPG-----TFC-RKYNPVCKSCPPSTFFSIG 56  
Db 12 LLLGLSLGTVTKLNCVKDTPSGHKCCRCQPGHGMVSRCDHTRDTVCHPCPEPGFYNEAV 71  
QY 57 QPNPNCNCRVC--AGYFRFKKFCSSTHNAECEIEG-----FHCLGPQCTRCEKDCRP 107  
Db 72 NYDTCKQCTQCNRHRSSELKQNCPTPTEDTVQCRRPGTQPRQDSSHKLGVDCV----PCPP 127  
QY 108 GQELTKQCKTCSLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP----- 160  
Db 128 GH-----FSPGSNQACKPWTNCTLSGKQIRHPASNSLDTVCEDRSLLATL 172  
QY 161 -----PVVSFSPSTTISVTPG-----GPGGHSLSQVLTFLAL 193  
Db 173 LWETQRTTFRPTTVPTTVPRTSQLPSTPTLVAPEGPAFAVILGLGLLAPLTVLLAL 232

RESULT 12  
A49053  
CD27 antigen precursor - mouse  
N;Alternate names: CD27L receptor; T cell activation antigen CD27  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Dec-1993 #sequence\_revision 22-Apr-1995 #text\_change 11-Sep-1998  
C;Accession: A49053  
R;Gravestein, L.A.; Blom, B.; Nolten, L.A.; de Vries, E.; van der Horst, G.; Ossendorp, P.  
Eur. J. Immunol. 23, 943-950, 1993  
A;Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte  
A;Reference number: A49053; MUID:93209296; PMID:8384562  
A;Accession: A49053  
A;Molecule type: mRNA  
A;Residues: 1-250 <GRA>  
A;Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBIP:128169)

C;Superfamily: CD27 antigen; NGF receptor repeat homology  
 C;Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; tra  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-250/Product: CD27 antigen #status predicted <MAT>  
 F;21-182/Domain: extracellular #status predicted <EXT>  
 F;27-63/Domain: NGF receptor repeat homology <NG1>  
 F;65-105/Domain: NGF receptor repeat homology <NG2>  
 F;121-179/Region: proline/serine/threonine-rich  
 F;183-202/Domain: transmembrane #status predicted <TMN>  
 F;203-250/Domain: intracellular #status predicted <INT>  
 F;95,162/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.9%; Score 169.5; DB 1; Length 250;  
 Best Local Similarity 27.0%; Pred. No. 1.6e-05;  
 Matches 62; Conservative 29; Mismatches 94; Indels 45; Gaps 11;

QY 28 CDNCQPGTF----CRKYNPV--CKSCPPST-FS-SIGQPNICRVACGYFRFKKFCSS 79  
 Db 40 CRMCEPGTFFVKDCEQDRTAAQCDPCIPGTSFSDYHTRPHCESCRHCNSGFLIRN-CTV 98  
 QY 80 THNAECECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCSLGTFTNDQNGTGVCRPWTNC 139  
 Db 99 TANAECSCSKWQCRDQECTCDPLNPA--LTRQSETPSPQ-----PPTH- 144  
 QY 140 SLDGRSVLKTGTTEKDVVCGPPVVSFSPSTISVTPEGGGSHSLQVLTFLALTSALLL 199  
 Db 145 -----LPHGTEKPSW-----PLHRQLPNTVYSQSSSRPLCSDDCIRIFVTFSSMFLI 193  
 QY 200 ALIFITLLFSVLKWKIRKPPHIFKQPKKTTGAQAEEDACSCRCQREEG 249  
 Db 194 FVLGAILFFHQR--RNHGPNEDRQ-----AVPEECPYSCPREEG 232

## RESULT 13

A46517  
 CD27 antigen precursor - human  
 N;Alternate names: CD27L receptor; T cell activation antigen CD27  
 C;Species: Homo sapiens (man)  
 C;Date: 18-Jun-1993 #sequence\_revision 22-Apr-1995 #text\_change 22-Jun-1999  
 C;Accession: A46517; A46454  
 R;Loenen, W.A.; Gravesstein, L.A.; Beumer, S.; Melief, C.J.; Hagemeijer, A.; Borst, J.  
 J. Immunol. 149, 3937-3943, 1992  
 A;Title: Genomic organization and chromosomal localization of the human CD27 gene.  
 A;Reference number: A46517; MUID:93094588; PMID:1334106  
 A;Accession: A46517  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-260 <LOE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:120386)  
 A;Note: authors propose an alternative repeat pattern  
 R;Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B.  
 J. Immunol. 147, 3165-3169, 1991  
 A;Title: The T cell activation antigen CD27 is a member of the nerve growth factor/tumor  
 A;Reference number: A46454; MUID:92013149; PMID:1655907  
 A;Accession: A46454  
 A;Molecule type: mRNA  
 A;Residues: 1-58, 'A', 60-260 <CAM>  
 A;Cross-references: GB:M63928; NID:g180084; PIDN:AAA58411.1; PID:g180085  
 A;Note: sequence extracted from NCBI backbone (NCBIN:60285, NCBIP:60289)  
 C;Comment: A soluble CD27 found in serum and urine is formed by proteolysis.  
 C;Genetics:  
 A;Gene: GDB:CD27  
 A;Cross-references: GDB:132582; OMIM:186711  
 A;Map position: 12p13-12p13  
 A;Introns: 46/1; 90/1; 150/1; 180/1; 220/1  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology  
 C;Keywords: duplication; glycoprotein; homodimer; phosphoprotein; receptor; surface anti  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-260/Product: CD27 antigen #status predicted <MAT>  
 F;21-191/Domain: extracellular #status predicted <EXT>  
 F;27-63/Domain: NGF receptor repeat homology <NG1>  
 F;65-105/Domain: NGF receptor repeat homology <NG2>  
 F;121-188/Region: proline/serine/threonine-rich

F;192-211/Domain: transmembrane #status predicted <TMN>  
 F;212-260/Domain: intracellular #status predicted <INT>  
 F;95/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.7%; Score 166.5; DB 1; Length 260;  
 Best Local Similarity 25.0%; Pred. No. 2.7e-05;  
 Matches 63; Conservative 25; Mismatches 85; Indels 79; Gaps 12;

QY 28 CDNCQPGTF----CRKYNPV--CKSCPPS-TFS-SIGQPNICRVACGYFRFKKFCSS 79  
 Db 40 COMCEPGTFLVKDCDQHRKTAQCDPCIPGVSPSPDHTTRPHCESCRHCNSGLLVN-CTI 98  
 QY 80 THNAECECIEGFHCLGPQCTRCCKDCRPGQELTKQGCKTCSLGTFTNDQNGTGVCRPWTNC 139  
 Db 99 TANAECACRNGWQCRDKECTCD-----PLPNP 126  
 QY 140 SLDGRSVLKTGTTEKDVVCGPPVVSFSPST-----ISVTPEGGGSHSLQVLTFLAL-- 193  
 Db 127 SLTARS-----SQALSPHPQTHLPYVSEMLEARTAGH-MQTLADFRQLPA 171  
 QY 194 -----TSALLLALIFITLLFSVLKWKIRKPPHIFKQPKKTTGAQAEEDAC 239  
 Db 172 RTLSTHWPQQRSCLSSDFIRILVIFSGMFLVFTLAGALFLH-QRRKYSNKGESPVPEAE 230  
 QY 240 SCR--CPQEEEG 249  
 Db 231 PCRYSCPREEG 242

## RESULT 14

I48700  
 Gene ox40 protein - mouse  
 N;Alternate names: OX40 antigen  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
 C;Accession: I48700; I48334; S34377  
 R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.; H  
 J. Immunol. 151, 5261-5271, 1993  
 A;Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell inte  
 A;Reference number: I48700; MUID:94044750; PMID:8228223  
 A;Accession: I48700  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-272 <RES>  
 A;Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828  
 R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.  
 Eur. J. Immunol. 25, 926-930, 1995  
 A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40  
 A;Reference number: I48334; MUID:95255413; PMID:7737295  
 A;Accession: I48334  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-14, 'G', 16-272 <RE2>  
 A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAAS9476.1; PID:g732819  
 C;Genetics:  
 A;Gene: ox40  
 A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1  
 C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 11.1%; Score 158; DB 2; Length 272;  
 Best Local Similarity 23.8%; Pred. No. 0.00012;  
 Matches 57; Conservative 25; Mismatches 87; Indels 70; Gaps 10;

QY 8 VVIVILLVGEKVGAVQNS-----CDNCQPG-----TFC-RKYNPVCKSCPSTPSSI 55  
 Db 12 LLLALTGLVTARRLNCVKHTYPSGKCCRECPQPGHGMVSRCDHTDRLCHPCETGFYNEA 71  
 QY 56 GGQPNICRVACGYFRFKKFCSSSTHNAECECIEGFHCLGPQCTRCCKDCRPGQELTKQG 115  
 Db 72 VNYDTCKQCTQC-----NHRSGSELKQ--NCTPTQDTCR--CRPGTQPRQDS 115  
 QY 116 -----CKTCSLGTFTNDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVWCGP----- 160

Db 116 GYKLGVDVCPGPHGSPNNQ-ACKPWTNCTLSGKQTRHPASDSLDVACEDRSLLATLL 174

QY 161 -----PVVSFSPSTTISVTPEG-----GPGGHSLOVLTFLAL 193

Db 175 WETQPTFTTQSTTVWPRISLPSPPTLVTPGPAFAVLLGLGLLAPLTVLLAL 233

RESULT 15

D72175

G2R protein - variola minor virus (strain Garcia-1966)

C;Species: variola minor virus

C;Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 15-Sep-2003

C;Accession: D72175

R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopan

submitted to GenBank, March 1998

A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor

A;Reference number: A72150

A;Accession: D72175

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-349 <SHC>

A;Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G5830759

A;Experimental source: strain Garcia-1966

C;Genetics:

A;Gene: G2R

C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 9.9%; Score 142; DB 2; Length 349;

Best Local Similarity 23.0%; Pred. No. 0.0022;

Matches 60; Conservative 28; Mismatches 103; Indels 70; Gaps 11;

QY 28 CDNCQPGTFC-----RKYNPVCKSCPPSTFSSIGGQ-PNCNICR-VCAGYFRFKFCSST 80

Db 44 CLSCPPGTYSASLCLDSKNTQCTPCGSGTFTSRNHLPACLSCNCRNSNQVETRSCNTT 103

QY 81 HNAECEIEGFHCL---GPQTRCEKDCRFQELTKQG-----CKTCSLGTFN-DQN 128

Db 104 HNRICECSPGYCLLKSGSGKACVSTQKCGIGYGVSGHTSVGDVICSFGFTGYSYTVS 163

QY 129 GTGVCPRPWTNCSLDGRSVLKTGTEKDVVCCPPVVSFSPSTTISVTPEGGPGHSLQVLT 188

Db 164 STDKCEPVNNTFNVIDEITLVPVNDTSC-----TFTTTGLSES----- 204

QY 189 LFLALTSALLLAL-----IFITLLFSVLKWI-----RKFPHPFK----- 223

Db 205 ---ILTSELITMNTHTDCNPVREYFVSLNKVATSGFTGTENRYQNSKVCTLNFEIKC 261

QY 224 ----QPFKKTGAAQEEEDACS 240

Db 262 NKGSSFKQLTKAKNDGMS 282

RESULT 16

B43692

T2 protein - rabbit fibroma virus

C;Species: rabbit fibroma virus, Shope fibroma virus

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Sep-2003

C;Accession: B43692

R;Upton, C.; Delange, A.M.; McFadden, G.

Virology 160, 20-30, 1987

A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric

A;Reference number: A43692; MUID:87321103; PMID:2820128

A;Accession: B43692

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 <UPT>

A;Cross-references: GB:M17433

C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

F;64-105/Domain: NGF receptor repeat homology <NG2>

F;106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 9.8%; Score 140.5; DB 2; Length 325;

Best Local Similarity 27.6%; Pred. No. 0.0026;

Matches 43; Conservative 12; Mismatches 54; Indels 47; Gaps 8;

QY 28 CDNCQPGTFCRKY-----NPVCKSCPPSTP-SSIGGQPNICR-VCAGYFRFKFCSST 80

Db 40 CASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCGPGCTGHLSESQPCDRT 99

QY 81 HNAECEIEGFHCLGPQTRCEKDCRFQELTKQGCKTCSLGTFTNDQNGTVCRCPTWNC- 139

Db 100 HDRVCNCSGTNYCL-----LKGQNGCRICAPQTKCP 130

QY 140 ---SLDGRSVLKTGTT--EKDVVCGPPVVSFSPSTT 170

Db 131 AGYGVSGHT--RAGDTLCEK--CPHTYSDSLST 161

RESULT 17

JN0006

nerve growth factor receptor, low affinity precursor - chicken

N;Alternate names: NGF receptor

C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C;Accession: JN0006; A60504

R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reich

Neuron 2, 1123-1134, 1989

A;Title: Structure and developmental expression of the nerve growth factor receptor in t

A;Reference number: JN0006; MUID:90166579; PMID:2560385

A;Accession: JN0006

A;Molecule type: mRNA

A;Residues: 1-416 <LAR>

A;Experimental source: embryonic chick brain

R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.

Dev. Biol. 137, 287-304, 1990

A;Title: Structure and developmental expression of the chicken NGF receptor.

A;Reference number: A60504; MUID:90152140; PMID:2154393

A;Accession: A60504

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>

C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma ce

C;Comment: The cysteine-rich region of the extracellular domain may form part or all of t

C;Comment: This protein is thought to form a high-affinity receptor when it associates w

C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-416/Product: nerve growth factor receptor #status predicted <EXT>

F;21-239/Domain: extracellular #status predicted <EXT>

F;24-57/Domain: NGF receptor repeat homology <NG1>

F;59-100/Domain: NGF receptor repeat homology <NG2>

F;101-139/Domain: NGF receptor repeat homology <NG3>

F;141-181/Domain: NGF receptor repeat homology <NG4>

F;189-237/Region: serine/threonine-rich

F;240-261/Domain: transmembrane #status predicted <MEM>

F;262-416/Domain: intracellular #status predicted <INT>

F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.8%; Score 139.5; DB 1; Length 416;

Best Local Similarity 25.7%; Pred. No. 0.0038;

Matches 53; Conservative 24; Mismatches 82; Indels 47; Gaps 12;

QY 9 WVIVLLVGEKVGAVQNSCDNC-----QPGTFCRKYN-----PVCKSCPP 49

Db 5 VPLLLLLL---PAGPTWGSKEKCLTKMYTTSGECKACNLGEGVQVPCGVNQTVCPECLD 61

QY 50 S-TFS-SIGGQPNICRVCAGYFRFKFCSSTHNAECEIEGF-----HCLGPQCTR 100

Db 62 SVTYSDTVSAPECKPCTQCVGLHMSAPCVESDDAVCRCAVGYFQDELSGSC--KECSI 119

QY 101 CEK-----DCRPGQELTKQGCKTCSLGTFTNDQ-NGTGVCRPWTNCSLDGRSVLKTGTE 153

Db 120 CEVGFGLMFPCRDSDQTV---CECEPGETFSDANFVDPCLPTICE-ENEVMVKECTAT 175

QY 154 KDVVC---GPPVVSFSPSTTISVTPE 176



A;Cross-references: EMBL:X69869; NID:G53055; PIDN:CAA9502.1; PID:G53056  
 C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
 C;Function:  
 A;Description: Interact with cells and with other basement membrane proteins to promote  
 C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h  
 C;Keywords: basement membrane; calcium binding; coiled coil; extracellular matrix; glyco  
 F;1-22/Domain: signal sequence #status predicted <SIG>  
 F;23-3106/Product: laminin alpha-2 chain #status predicted <MAT>  
 F;283-337/Domain: laminin-type EGF-like homology <LE01>  
 F;340-407/Domain: laminin-type EGF-like homology <LE02>  
 F;410-462/Domain: laminin-type EGF-like homology <LE03>  
 F;465-511/Domain: laminin-type EGF-like homology <LE04>  
 F;514-523/Domain: laminin-type EGF-like homology #status atypical <LE05>  
 F;720-750/Domain: laminin-type EGF-like homology <LE06>  
 F;753-800/Domain: laminin-type EGF-like homology <LE07>  
 F;803-858/Domain: laminin-type EGF-like homology <LE08>  
 F;861-911/Domain: laminin-type EGF-like homology <LE09>  
 F;914-960/Domain: laminin-type EGF-like homology <LE10>  
 F;963-1007/Domain: laminin-type EGF-like homology <LE11>  
 F;1010-1053/Domain: laminin-type EGF-like homology <LE12>  
 F;1056-1099/Domain: laminin-type EGF-like homology <LE13>  
 F;1102-1121/Domain: laminin-type EGF-like homology #status atypical <LE14>  
 F;1123-1159/Domain: laminin-type EGF-like homology #status atypical <LE15>  
 F;1162-1171/Domain: laminin-type EGF-like homology #status atypical <LE16>  
 F;1376-1413/Domain: laminin-type EGF-like homology #status atypical <LE17>  
 F;1416-1462/Domain: laminin-type EGF-like homology <LE18>  
 F;1465-1520/Domain: laminin-type EGF-like homology <LE19>  
 F;1523-1567/Domain: laminin-type EGF-like homology <LE20>  
 F;2166-2327/Domain: laminin G repeat homology <LG1>  
 F;2360-2520/Domain: laminin G repeat homology <LG2>  
 F;2546-2709/Domain: laminin G repeat homology <LG3>  
 F;2785-2933/Domain: laminin G repeat homology <LG4>  
 F;2960-3106/Domain: laminin G repeat homology <LG5>

Query Match 9.7%; Score 138; DB 1; Length 3106;  
 Best Local Similarity 26.7%; Pred. No. 0.024;  
 Matches 54; Conservative 19; Mismatches 67; Indels 62; Gaps 13;

QY 23 AVONSCDN-----CQGTFCRKNVPVCKSCPPSTFSSIGQPNICRVKVCAGYFRPKK 75  
 DB 870 SIPGSCDLSGSLICKPGTGR----YCELCADGYFGDAVNTKNCQPCR-CDINGSPSE 924

QY 76 FCSSTHNAEC-----IEGFHC-----LGPQCTRCKD-----C 105  
 DB 925 DC-HRTGQCECRPNVQGRHCDCKPETFGQLGRGLPCNCSFSGSKSFDCEASGQWC 983

QY 106 RPOELTKQCKTCSLGTDFNDQNGTGVCRPWNCS-LDGRSVLKTGTEKDWVCGPPVVS 164  
 DB 984 QPG--VAGKKCDRCAGYFNFQEGGCI-----CDCSHLGNNDPKTG-----QCIC----- 1028

QY 165 FSPSTTISVTPEGPG--GHSL 184  
 DB 1029 -PNTTGEKCECLPNTWGHSI 1049

RESULT 21  
 A35502  
 major surface-labeled trophozoite antigen precursor - Giardia lamblia  
 C;Species: Giardia lamblia  
 C;Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 09-Sep-1997  
 C;Accession: A35502  
 R;Gilllin, F.D.; Hagblom, P.; Harwood, J.; Aley, S.B.; Reiner, D.S.; McCaffery, M.; So, M  
 Proc. Natl. Acad. Sci. U.S.A. 87, 4463-4467, 1990  
 A;Title: Isolation and expression of the gene for a major surface protein of Giardia lam  
 A;Reference number: A35502; MUID:90280395; PMID:2352929  
 A;Accession: A35502  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-713 <GIL>  
 A;Cross-references: GB:M33641; NID:g159131; PID:g159132  
 C;Keywords: surface antigen; transmembrane protein

Query Match 9.5%; Score 135.5; DB 2; Length 713;

Best Local Similarity 25.6%; Pred. No. 0.011;  
 Matches 58; Conservative 20; Mismatches 67; Indels 82; Gaps 15;

QY 15 LVGCE-----KVGAVQNSCD--NCQ-PGTFRC-----KYNPVCKSCPPSTFSSIGGQ 58  
 DB 312 LVTCSACTDGYKPSADTKTCEAVSNCKTPG--CKACNEGKENEVCTDCDGSYLTPTSQ 369

QY 59 PNC-NICRVACAGYF----RFKKFCSSTHNAECE-----CIEGFHCLGPQCTRCEK 103  
 DB 370 --CIDSCAKIGNYYGATEGAKKLCKEATAANCKTCDDQGCQACNDGFYKNGDACSPCH- 426

QY 104 DCRPGQELTKQCKTCSLGTDFND-----QNGTGVCVRPW 136  
 DB 427 -----ESCKTCSAGTASDCTEPTGKALRYGDDGKTGTCGEGCTTGTGAGACK-- 474

QY 137 TNCSL--DCRSVLK--TGTTE--KDVVCGPPVVSFSPSTTISVTPEG 177  
 DB 475 -TCGLTIDGASYCSECATTEYPQNGVCAKASRATPTCNDSPIQNG 520

# RESULT 22

GQHUN  
 nerve growth factor receptor precursor, low affinity [validated] - human  
 N;Alternate names: NGF receptor  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 08-Dec-2000  
 C;Accession: A25218; A60204; S21689; I57638  
 R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.;  
 Cell 47, 545-554, 1986  
 A;Title: Expression and structure of the human NGF receptor.  
 A;Reference number: A25218; MUID:87051725; PMID:3022937  
 A;Accession: A25218  
 A;Molecule type: mRNA  
 A;Residues: 1-427 <JOH>  
 A;Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205  
 R;Marano, N.; Dietzschold, B.; Barley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;  
 J. Neurochem. 48, 225-232, 1987  
 A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factor  
 A;Reference number: A60204; MUID:87085574; PMID:3025363  
 A;Accession: A60204  
 A;Molecule type: protein  
 A;Residues: 29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 <MAR>  
 A;Experimental source: melanoma cell line A875  
 A;Note: this sequence has been corrected by a note added in proof to follow the nucleotic  
 R;Visavajjalala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.  
 Arch. Biochem. Biophys. 294, 244-252, 1992  
 A;Title: Structural domains of the extracellular domain of human nerve growth factor rece  
 A;Reference number: S21689; MUID:92198017; PMID:1372492  
 A;Accession: S21689  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 183-208 <VIS>  
 R;Sehgal, A.; Patil, N.; Chao, M.  
 Mol. Cell. Biol. 8, 3160-3167, 1988  
 A;Title: A constitutive promoter directs expression of the nerve growth factor receptor  
 A;Reference number: I57638; MUID:89096903; PMID:2850481  
 A;Accession: I57638  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-22 <RES>  
 A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207  
 C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma ce  
 C;Comment: The cysteine-rich region of the extracellular domain may form part or all of t  
 C;Comment: This protein is thought to form a high-affinity receptor when it associates w  
 C;Comment: This receptor undergoes both N- and O-linked glycosylation.  
 C;Genetics:  
 A;Gene: GDB:NGFR  
 A;Cross-references: GDB:120234; OMIM:162010  
 A;Map position: 17q21-17q22  
 C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; tr  
 F;1-28/Domain: signal sequence #status predicted <SIG>  
 F;29-427/Product: nerve growth factor receptor #status experimental <MAT>

F;29-250/Domain: extracellular #status predicted <EXT>  
F;32-65/Domain: NGF receptor repeat homology <NG1>  
F;67-108/Domain: NGF receptor repeat homology <NG2>  
F;109-147/Domain: NGF receptor repeat homology <NG3>  
F;149-189/Domain: NGF receptor repeat homology <NG4>  
F;197-248/Region: serine/threonine-rich  
F;251-272/Domain: transmembrane #status predicted <TRM>  
F;273-427/Domain: intracellular #status predicted <INT>  
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.5%; Score 135; DB 1; Length 427;  
Best Local Similarity 25.2%; Pred. No. 0.0083;  
Matches 65; Conservative 26; Mismatches 97; Indels 70; Gaps 15;  
QY 10 VIVLLVGCCKVAVQ-----NSCDNCQPGTF-----CRKYNPVCKSCPPS-TFS 53  
Db 15 LLLLLLVSLGGAKEACTGLYTHSGECKACNLGEGVAQPCGANQTVCEPCLDSVTF 74  
QY 54 S-IGQPNICNCRVCAGYFRFKKFCSSSTHNAFCECIEGFHCLGPOCTRCE--KDCRPGQE 110  
Db 75 DVVSATEPCPKCTECVGLQSMAPCVAEDDAVCRCAAGYV-QDETTGRCEACRVCEAGSG 133  
QY 111 LT-----KQG--CKTCSLGTENDQ-NGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC----- 158  
Db 134 LVFSCQDKQNTVCEECFDTGYSDEANHVDPCLPCTVCE-DTERQLRECFRWADAEEELP 192  
QY 159 -----GPPVVSFS--PSTTISVTPEGGPG-----GHSLOVLT----- 188  
Db 193 GRWITRSTPPEGSDSTAPSTQ---EPEAPPEQDLIASTVAGVTTVMGSSQPVVTRGTTD 249  
QY 189 -----LFLALTSALLALI 202  
Db 250 NLIPVYCSILA VVGLV 267

## RESULT 23

JC2005  
Integrin beta-5 chain - baboon  
C;Species: Papio sp. (baboon)  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 21-Jan-2000  
C;Accession: JC2005  
R;Shoji, M.; Hayzer, D.J.; Kim, T.M.; Runge, M.S.; Hanson, S.R.  
Gene 133, 307-308, 1993  
A;Title: Human and baboon integrin beta 5 subunit-encoding mRNAs have alternative polyad  
A;Reference number: JC2005; MUID:94040831; PMID:8224922  
A;Accession: JC2005  
A;Molecule type: mRNA  
A;Residues: 1-656 <SHO>  
A;Note: the authors translated the codon AGA for residue 454 as Lys, CAA for residue 471  
C;Comment: This protein is a predominant subunit for the vitronectin receptor in baboon  
C;Superfamily: integrin beta chain; laminin-type EGF-like homology  
C;Keywords: cell adhesion  
F;320-370/Domain: laminin-type EGF-like homology <LEG>

Query Match 9.5%; Score 135; DB 2; Length 656;  
Best Local Similarity 27.7%; Pred. No. 0.012;  
Matches 64; Conservative 30; Mismatches 93; Indels 44; Gaps 14;  
QY 27 SCDNCQ--PGTFCRKYNPVCK-----SCP--PSTFSSIGGQPNICRVACAGYFRFKKFC 78  
Db 386 SCNQCSCFSEFGKIYGFCECDNFSCARNKGVLCGSGHGECHGECKCHAGYIGDNCNC- 444  
QY 79 STHNAECE-----CIEGFHCLGPQC-----TRCEK--DCRPGQELTKQCKTCSL 121  
Db 445 STDISTCRGRDQICSERGHCLCGQCCTEPGAFGEMCEKCPCTC-PDACSTKRDCEVCPL 503  
QY 122 ---GTFNDQNGTGVCR---PWTNCSL--DGRSVLKTGTTEKDVVCGPPV---SFSPT 169  
Db 504 LHSGKPDNQCHSLCRDEVITWVDIVKDDQEAFLCYFKTAKDCVMFTYVELPSGKSNL 563  
QY 170 TISVTPGPGGHSLOVLTFLALTSALLLALIFITLLFSVLKWI--RKXF 218  
Db 564 TVLREPE---CGNTPNAMTILLAVVGSILLVGLALLAIWKLVITIHDRREF 611

## RESULT 24

A38308  
Integrin beta-5 chain precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 20-Aug-1999  
C;Accession: A38308; A35775; S12534; S11708  
R;McLean, J.W.; Vestal, D.J.; Cheresh, D.A.; Bodary, S.C.  
J. Biol. Chem. 265, 17126-17131, 1990  
A;Title: CDNA sequence of the human integrin beta-5 subunit.  
A;Reference number: A38308; MUID:91009141; PMID:2211615  
A;Accession: A38308  
A;Molecule type: mRNA  
A;Residues: 1-799 <MCL>  
A;Cross-references: GB:J05633; NID:gl86504; PIDN:AAA59183.1; PID:gl86505  
A;Note: parts of this sequence, including the amino end of the mature protein, were confi  
R;Suzuki, S.; Huang, Z.S.; Tanihara, H.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5354-5358, 1990  
A;Title: Cloning of an integrin beta subunit exhibiting high homology with integrin beta-  
A;Reference number: A35775; MUID:90319111; PMID:2371275  
A;Accession: A35775  
A;Molecule type: mRNA  
A;Residues: 1-192, 'A', 194-644, 'L', 646-789, 793-799 <SUZ>  
A;Cross-references: GB:M35011; NID:gl84524; PIDN:AAA52707.1; PID:g306894  
R;Ramawamy, H.; Hemler, M.E.  
EMBO J. 9, 1561-1568, 1990  
A;Title: Cloning, primary structure and properties of a novel human integrin beta subunit  
A;Reference number: S12534; MUID:90228356; PMID:2328726  
A;Accession: S12534  
A;Molecule type: mRNA  
A;Residues: 1-644, 'L', 646-799 <RAM>  
A;Cross-references: EMBL:X53002; NID:G333952; PIDN:CAA37188.1; PID:g333953  
C;Genetics:

A;Gene: GDB:ITGB5  
A;Cross-references: GDB:128005; OMIM:147561  
A;Map position: 17q11-17qter  
C;Superfamily: integrin beta chain; laminin-type EGF-like homology  
C;Keywords: cell adhesion; cytoskeleton; duplication; extracellular matrix; glycoprotein;  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-799/Product: integrin beta-5 chain #status experimental <MAT>  
F;25-719/Domain: extracellular #status predicted <EXT>  
F;463-513/Domain: laminin-type EGF-like homology <LEG>  
F;720-742/Domain: transmembrane #status predicted <TMM>  
F;743-799/Domain: intracellular #status predicted <INT>  
F;347,460,477,505,552,586,654,705/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 9.5%; Score 135; DB 2; Length 799;  
Best Local Similarity 27.7%; Pred. No. 0.014;  
Matches 64; Conservative 30; Mismatches 93; Indels 44; Gaps 14;

QY 27 SCDNCQ--PGTFCRKYNPVCK-----SCP--PSTFSSIGGQPNICRVACAGYFRFKKFC 78  
Db 529 SCNQCSCFSEFGKIYGFCECDNFSCARNKGVLCGSGHGECHGECKCHAGYIGDNCNC- 587  
QY 79 STHNAECE-----CIEGFHCLGPQC-----TRCEK--DCRPGQELTKQCKTCSL 121  
Db 588 STDISTCRGRDQICSERGHCLCGQCCTEPGAFGEMCEKCPCTC-PDACSTKRDCEVCPL 646  
QY 122 ---GTFNDQNGTGVCR---PWTNCSL--DGRSVLKTGTTEKDVVCGPPV---SFSPT 169  
Db 647 LHSGKPDNQCHSLCRDEVITWVDIVKDDQEAFLCYFKTAKDCVMFTYVELPSGKSNL 706  
QY 170 TISVTPGPGGHSLOVLTFLALTSALLLALIFITLLFSVLKWI--RKXF 218  
Db 707 TVLREPE---CGNTPNAMTILLAVVGSILLVGLALLAIWKLVITIHDRREF 754

## RESULT 25

A26431  
nerve growth factor receptor precursor, low affinity - rat  
N;Alternate names: NGF receptor  
C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: A26431; PH1229  
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
Nature 325, 593-597, 1987  
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.  
A;Reference number: A26431; MUID:87115859; PMID:3027580  
A;Accession: A26431  
A;Molecule type: mRNA  
A;Residues: 1-425 <RAD>  
A;Cross-references: GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756  
R;Metsis, M.; Timmusk, T.; Allikmets, R.; Saarna, M.; Persson, H.  
Gene 121, 247-254, 1992  
A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoid  
A;Reference number: PH1229; MUID:93077038; PMID:1446821  
A;Accession: PH1229  
A;Molecule type: DNA  
A;Residues: 1-20 <MET>  
A;Cross-references: GB:X61269  
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C;Comment: This protein is thought to form a high-affinity receptor when it associates w  
C;Genetics:  
A;Introns: 20/3  
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-425/Product: nerve growth factor receptor #status predicted <MAT>  
F;30-251/Domain: extracellular #status predicted <EXT>  
F;33-66/Domain: NGF receptor repeat homology <NG1>  
F;68-109/Domain: NGF receptor repeat homology <NG2>  
F;110-148/Domain: NGF receptor repeat homology <NG3>  
F;150-190/Domain: NGF receptor repeat homology <NG4>  
F;198-249/Region: serine/threonine-rich  
F;252-273/Domain: transmembrane #status predicted <MEM>  
F;274-425/Domain: intracellular #status predicted <INT>  
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.3%; Score 133; DB 1; Length 425;  
Best Local Similarity 25.6%; Pred. No. 0.012;  
Matches 51; Conservative 20; Mismatches 88; Indels 40; Gaps 11;

Qy 10 VIVLLVGEKVGAVQ-----NSCDNCPQGTGTF-----CRKNPVCKSCPPS-IFS 53  
Db LLLLLLILGVSSGAKETCTGLYTHSGECKKACNLGEGVAQPCGANQTVCEPCLDNVTF 75  
Qy 54 S-IGGPNICNCRVAGYFRFKFCSSTHNAECIEGF-----HCLGPQCTRCCK-- 103  
Db DVVSATPECKPCTECLGLQMSAPCVAEADAVCRCAVGYQDEBTGHC--EACSVCEVGS 133  
Qy 104 ---DCRPGQELTKQCKTCSLGFNDQ-NGTGVCPRWTNCSLDGRSVLTKGTTEKDVVC 158  
Db 134 GLVFSQDKQNTV---CEECEPGYSDANVHDPCLPCTVCE-DTERQLRECTPWADABC 189  
Qy 159 GPPVVSFPSTTISVTPEG 177  
Db 190 EEIPGRWIPRST---PPEG 205

RESULT 26  
QVZML  
T2 protein - myxoma virus (strain Lausanne)  
C;Species: myxoma virus  
C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 15-Sep-2003  
C;Accession: A40566  
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.  
Virology 184, 370-382, 1991  
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis f  
A;Reference number: A40566; MUID:91335768; PMID:1651597  
A;Accession: A40566  
A;Molecule type: DNA  
A;Residues: 1-326 <UPT>  
A;Cross-references: GB:M95181; GB:M37976; NID:G332309; PIDN:AAA46632.1; PID:G332310  
C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

C;Keywords: glycoprotein  
F;64-105/Domain: NGF receptor repeat homology <NG2>  
F;106-147/Domain: NGF receptor repeat homology <NG3>  
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 130.5; DB 1; Length 326;  
Best Local Similarity 25.8%; Pred. No. 0.014;  
Matches 41; Conservative 22; Mismatches 49; Indels 47; Gaps 10;

Qy 28 CDNCPQGTFCRKY-----NPVCKSCPSTF-SSIGQPNICR-VCAGYFRFKFCSST 80  
Db 40 CTSCPPGVSASRLCGPSDTCSPCKNETFTASTNHAPACVSCRCCTGHLSESQCDKT 99  
Qy 81 HNAECEIEGFHCLGPQCTRCCKDCRPGQELTKQCKTCSLGFNDQNGTGVCPRWTNC- 139  
Db 100 RDRVCDCSAGNYCL-----LKGQE-----GCR-----ICAPKTKCP 130  
Qy 140 ---SLDGRSVLTKGTTEKDVVCGP-PVVSFSPSTTISVT 174  
Db 131 AGYGVSGHT--RTG----DVLTCKCPRYTYSDAVSSTET 163

RESULT 27  
A55677  
laminin beta-2 chain precursor (version 1) - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 17-Mar-1999  
C;Accession: A55677  
R;Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champiaud, M.F.;  
Genomics 24, 243-252, 1994  
A;Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal local  
A;Reference number: A55677; MUID:95213013; PMID:7698745  
A;Accession: A55677  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-1797 <WEW>  
A;Cross-references: GB:X79683  
C;Genetics:  
A;Gene: GDB:LAMB2  
A;Cross-references: GDB:132363; OMIM:150325  
A;Map position: 3p21.3-3p21.2  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer  
F;1-32/Domain: signal sequence #status predicted <SIG>  
F;33-1797/Product: laminin beta-2 chain #status predicted <MAT>  
F;283-344/Domain: laminin-type EGF-like homology <LE01>  
F;347-407/Domain: laminin-type EGF-like homology <LE02>  
F;410-467/Domain: laminin-type EGF-like homology <LE03>  
F;470-519/Domain: laminin-type EGF-like homology <LE04>  
F;522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F;783-828/Domain: laminin-type EGF-like homology <LE06>  
F;831-874/Domain: laminin-type EGF-like homology <LE07>  
F;877-924/Domain: laminin-type EGF-like homology <LE08>  
F;927-982/Domain: laminin-type EGF-like homology <LE09>  
F;985-1034/Domain: laminin-type EGF-like homology <LE10>  
F;1037-1091/Domain: laminin-type EGF-like homology <LE11>  
F;1094-1139/Domain: laminin-type EGF-like homology <LE12>  
F;1142-1186/Domain: laminin-type EGF-like homology <LE13>

Query Match 9.0%; Score 129; DB 2; Length 1797;  
Best Local Similarity 25.0%; Pred. No. 0.071;  
Matches 47; Conservative 13; Mismatches 46; Indels 82; Gaps 12;

Qy 20 KVGAVQNSCDNCPQGTFCRKNPV-CKSC---PPSTFSSI----- 55  
Db 805 KPGVWGRRCDCAPGY--GFGPTGCAQCQSPRGALSSLCERTSQCLCRTGAFGLRCD 862  
Qy 56 -----GGQPNICNCRVAGYFRFKFCSSTHNAEC-----ECIEGFH---- 92  
Db 863 ACQRGQWGFPSRCPC-VGNH---ADEC-NHTGACLGCRDLTGGEHCERCICAGFGDPR 917  
Qy 93 -CLGPQC-----TRCEKD-----CRPGQELTKQCKTCSLGTTFND 126

Db 918 LPYGAQCRPCPEPGSGRHFATSCHEYSQIIVCHCRAG--YTGLRCEACAPQFGD 975  
 QY 127 QNGTGVCR 134  
 Db 976 PSRPGACQ 983

RESULT 28  
 T10053  
 laminin alpha 5 chain - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2003  
 C;Accession: T10053  
 R;Miner, J.H.; Lewis, R.M.; Sanes, J.R.  
 submitted to the EMBL Data Library, November 1997  
 A;Reference number: Z16923  
 A;Accession: T10053  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-3635 <MIN>  
 A;Cross-references: EMBL:U37501; NID:G2599231; PID:G2599232  
 C;Genetics:  
 A;Gene: Lama5  
 C;Keywords: basement membrane; cell binding; extracellular matrix  
 F;1888-1939/Domain: laminin-type EGF-like homology <LEG>  
 F;1942-1970/Domain: EGF homology <EGF>

Query Match 9.0%; Score 129; DB 2; Length 3635;  
 Best Local Similarity 27.2%; Pred. No. 0.12;  
 Matches 63; Conservative 14; Mismatches 65; Indels 90; Gaps 17;  
 QY 27 SCNQCQGFPCRKYNPVC--KSCPPSTFSSIGGPN-----GN-ICRVACGYFRFKFCS 78  
 Db 1866 SCERCAPGFF--GNPLVLGSSCQPCDCSG-NGDPNMIFSDCDPLTGACRGCLR----- 1915  
 QY 79 STHNAECB-CIEGFH---CLGPQCRCEKDCRP-----GQELTK- 113  
 Db 1916 HTTGPHCERCAPGFYGNALLPNCNTRC--DCSPGCTETCDPQSGRCLCKAGVTGQRCDRC 1973  
 QY 114 -----QGCKTCSLG-----TFNDQNGTGVCRPWTNCSLDGRSVLKT-----GTT 152  
 Db 1974 LEGYFGFECQCGCRPCACGPAKGGCHPQSGQCHCQPGTT-----GPQCLCAPGYWGLP 2029  
 QY 153 EK-----DVVCG-----PPVVSFSPSTTIS-----VTPEGGPGGHS 184  
 Db 2030 EKGCRRCQCRGHCHDHTGHTCTCPGLSGERCDCSCQHQHVPVFGKPGGHGI 2081

RESULT 29  
 GQRTT1  
 tumor necrosis factor receptor 1 precursor - rat  
 N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999  
 C;Accession: B36555  
 R;Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
 DNA Cell Biol. 9, 705-715, 1990  
 A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor  
 A;Reference number: A36555; MUID:91090841; PMID:1702293  
 A;Accession: B36555  
 A;Molecule type: mRNA  
 A;Residues: 1-461 <HIM>  
 A;Cross-references: GB:M63122; NID:G207361; PIDN:AAA42256.1; PID:G207362  
 C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
 C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F;1-29/Domain: signal sequence #status predicted <SIG>  
 F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
 F;30-211/Domain: extracellular #status predicted <EXT>  
 F;30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>  
 F;44-82/Domain: NGF receptor repeat homology <NG1>  
 F;84-126/Domain: NGF receptor repeat homology <NG2>  
 F;127-167/Domain: NGF receptor repeat homology <NG3>

F;168-204/Domain: NGF receptor repeat homology <NG4>  
 F;212-234/Domain: transmembrane #status predicted <MEM>  
 F;235-461/Domain: intracellular #status predicted <INT>  
 F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 8.9%; Score 127; DB 1; Length 461;  
 Best Local Similarity 22.9%; Pred. No. 0.034;  
 Matches 58; Conservative 21; Mismatches 78; Indels 96; Gaps 11;  
 QY 14 LLVGCEKVGAVQNSCDNCPGTFPCRKNPV-----CKSCPPSTFSSIGGQPNCNICR--- 65  
 Db 68 LVSDCPSPGQ-ETVCEVCDKGTFTASQNHVRQCLSKCTCRKEMF-----QVEISPKADM 121  
 QY 66 --VC-AGYFRPKKFCSTH-----NACGCEIEGFHCLGPQCTR 100  
 Db 122 DTVCGCKKQFQRYLSETHFCQVDCSPCFNGTVPCKEKQNTVCNCHAGFFLSGNECTP 181  
 QY 101 CEKDCRPGQELTKQGCKTCSLGTFTNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGP 160  
 Db 182 C-SHCKKQECMK-----LCLP 197  
 QY 161 PVVSFSPSTTISVTPEGGGHSLOVLTFLALTSALLLALIFITLLFSLVKWIRKKKPPH 220  
 Db 198 PVA-----NVTNPQDSGTAVLLPLVIFLGL---CLFFICISLLCRYQWPRVYSI 246  
 QY 221 IFKQ--PFKXTTG 231  
 Db 247 ICRDSAPVKEVEG 259

RESULT 30  
 S18252  
 heparan sulfate proteoglycan - mouse  
 N;Alternate names: perlecan  
 C;Species: Mus musculus (house mouse)  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
 C;Accession: S18252; A31917; B31917; S66460  
 R;Noonan, D.M.; Fullen, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Hasse  
 J. Biol. Chem. 266, 22939-22947, 1991  
 A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogly  
 adhesion molecule.  
 A;Reference number: S18252; MUID:92078153; PMID:1744087  
 A;Accession: S18252  
 A;Molecule type: mRNA  
 A;Residues: 1-3707 <NOO>  
 A;Cross-references: EMBL:M77174; NID:G200295; PIDN:AAA39911.1; PID:G200296  
 R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hasse  
 J. Biol. Chem. 263, 16379-16387, 1988  
 A;Title: Identification of cDNA clones encoding different domains of the basement membrar  
 A;Reference number: A92680; MUID:89034110; PMID:2972708  
 A;Accession: A31917  
 A;Molecule type: mRNA  
 A;Residues: 940-1601 <NO2>  
 A;Cross-references: GB:J04054; NID:G200252; PIDN:AAA39899.1; PID:G200253  
 A;Accession: B31917  
 A;Molecule type: mRNA  
 A;Residues: 1870-2600 <NO3>  
 A;Cross-references: GB:J04055; NID:G200300; PIDN:AAA39912.1; PID:G200301  
 R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.  
 Eur. J. Biochem. 231, 551-556, 1995  
 A;Title: Structural properties of recombinant domain III-3 of perlecan containing a globu  
 A;Reference number: S66460; MUID:95377282; PMID:7649154  
 A;Accession: S66460  
 A;Molecule type: protein  
 A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>  
 C;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G repea  
 C;Keywords: glycoprotein  
 F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
 F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
 F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
 F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
 F;764-811/Domain: laminin-type EGF-like homology <LEG>  
 F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>

F;1563-1610/Domain: laminin-type EGF-like homology <EG7>  
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>  
F;3163-3198/Domain: EGF homology <EGF>  
F;3270-3423/Domain: laminin G repeat homology <LG2>  
F;3464-3492/Domain: EGF homology <EGF7>  
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      8.8%; Score 126; DB 2; Length 3707;  
Best Local Similarity 28.1%; Pred. No. 0.21;  
Matches 54; Conservative 14; Mismatches 66; Indels 58; Gaps 11;

QY    22   GAVNSCDNCQFG---TFCKYNPVCKSCPPSTFFSI-----GGQPNC-----NICRVC 67  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db    1535   GYGSLCQDCAPGYTRTGSGLYLGOCELCGNGHSDLCHPETGACSRCHNTAGEFCCLC 1594  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
QY    68   A-GYFRFKKFCSSHTNAECC-----IEGHCLGPQCCTCEKCDCRPQELTKQ 114  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db    1595   ATGYVGDATACTPEDCQPCACPLTNPNMFSRTCESLGAGGYRCTACE----PG--YTQG 1648  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
QY    115   GKTCISLGTENDON-GTGVCRRPWTNCSLDGRSVLKTCGTTEKDVVCGPPVVSFSPSTTISV 173  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db    1649   YCEQCAPGYEGDPNVQGRGCQLTKESLE-----VQHPSR--SV 1686  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
QY    174   TPEGGPGGHSLSQ 185  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
Db    1687   VPQGGP--HSLR 1696  
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 31  
MMMSA  
laminin alpha-1 chain precursor - mouse  
N;Alternate names: laminin chain A1  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 19-Jan-2001  
C;Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670  
R;Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.  
J. Biol. Chem. 263, 16536-16544, 1988  
A;Title: Laminin, a multidomain protein. The A chain has a unique globular domain and ho  
A;Reference number: A31771; MUID:89034134; PMID:3182802  
A;Accession: A31771  
A;Molecule type: mRNA  
A;Residues: 1-3084 <SAS>  
A;Cross-references: EMBL:J04064; NID:g309419; PIDN:AAA39410.1; PID:g309420  
A;Accession: A30449  
A;Molecule type: protein  
A;Residues: 183-195;570-571,'A',573-586;596-612,'X',614-617,'EMK';630-646;1217-1222,'YPH'  
2486;2624-2639;2818-2843;3009-3033,'V',3035 <SA2>  
R;Hartl, L.; Oberbaeumer, I.; Deutzmann, R.  
Eur. J. Biochem. 173, 629-635, 1988  
A;Title: The N terminus of laminin A chain is homologous to the B chains.  
A;Reference number: S00624; MUID:88225080; PMID:3267223  
A;Accession: S00624  
A;Molecule type: mRNA  
A;Residues: 1-208,'T',210-334 <HAR>  
A;Cross-references: EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID:g52858  
A;Accession: A30450  
A;Molecule type: protein  
A;Residues: 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',750-760,'G',762-763;  
3-1389;1449-1459 <HA2>  
A;Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-Ile  
R;Mann, K.; Deutzmann, R.; Timpl, R.  
Eur. J. Biochem. 178, 71-80, 1988  
A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th  
A;Reference number: S08895; MUID:89078415; PMID:2462498  
A;Accession: S08895  
A;Molecule type: protein  
A;Residues: 153-169 <MAN>  
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.  
Biochem. J. 252, 453-461, 1988  
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain  
A;Reference number: S02678; MUID:88326259; PMID:2458101  
A;Accession: S02678  
A;Molecule type: protein

A:Residues: 630-642,'D',644;2690-2704 <FUJ>  
R:Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.  
Eur. J. Biochem. 177, 35-45, 1988  
A:Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-ter  
A:Reference number: S01790; MUID:89030693; PMID:3181157  
A:Accession: S01790  
A:Molecule type: mRNA  
A:Residues: 2538-3084 <DEU>  
A:Cross-references: EMBL:X13459; NID:G55499; PIDN:CAA31807.1; PID:G818014  
A:Accession: A30451  
A:Molecule type: protein  
A:Residues: 1911-1929;1997-2006;2033-2045,'X',2047-2054,'X',2056-2066,'X',2068-2105;2120-  
470;2487-2498;2502-2525;2538-2557;2561-2591,'X',2593-2594;2600-2610;2616-2645;2648-2655;  
93;2998-3005,'A',3007-3033,'V',3035;3068-3083 <DE2>  
A:Note: 2256-Val was also found  
R:Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, J.  
Lab. Invest. 60, 772-782, 1989  
A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 chain  
A:Reference number: A34961; MUID:89280632; PMID:2733363  
A:Accession: S14670  
A:Molecule type: protein  
A:Residues: 2424-2436;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-26  
-2942,'T',2944-2964;2969-2976;2980-2993;2998-3000,'I',3002-3018,'V',3020-3034;3068-3083  
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C:Function:  
A:Description: Interact with cells and with other basement membrane proteins to promote C  
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like ho  
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-3084/Product: laminin alpha-1 chain #status predicted <MAT>  
F:25-277/Domain: VI <DOM6>  
F:277-331/Domain: laminin-type EGF-like homology <LE01>  
F:278-519/Domain: V <DOM5>  
F:334-401/Domain: laminin-type EGF-like homology <LE02>  
F:404-458/Domain: laminin-type EGF-like homology <LE03>  
F:461-507/Domain: laminin-type EGF-like homology <LE04>  
F:510-519/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F:520-715/Domain: IVb <DO4B>  
F:716-1166/Domain: IIib <DO3B>  
F:716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>  
F:749-795/Domain: laminin-type EGF-like homology <LE07>  
F:798-853/Domain: laminin-type EGF-like homology <LE08>  
F:830-834/Region: cell adhesion #status predicted  
F:856-906/Domain: laminin-type EGF-like homology <LE09>  
F:909-955/Domain: laminin-type EGF-like homology <LE10>  
F:958-1002/Domain: laminin-type EGF-like homology <LE11>  
F:1005-1048/Domain: laminin-type EGF-like homology <LE12>  
F:1051-1094/Domain: laminin-type EGF-like homology <LE13>  
F:1097-1116/Domain: laminin-type EGF-like homology #status atypical <LE14>  
F:1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>  
F:1147-1149/Region: cell attachment (R-G-D) motif  
F:1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>  
F:1167-1368/Domain: IVa <DO4A>  
F:1369-1561/Domain: IIIa <DO3A>  
F:1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>  
F:1410-1456/Domain: laminin-type EGF-like homology <LE18>  
F:1459-1513/Domain: laminin-type EGF-like homology <LE19>  
F:1516-1560/Domain: laminin-type EGF-like homology <LE20>  
F:1562-2133/Domain: II/I <DOM2>  
F:1562-2133/Region: heptad repeats  
F:2134-3084/Domain: G <DOMG>  
F:2150-2308/Domain: laminin G repeat homology <LG1>  
F:2337-2492/Domain: laminin G repeat homology <LG2>  
F:2518-2683/Domain: laminin G repeat homology <LG3>  
F:2748-2897/Domain: laminin G repeat homology <LG4>  
F:2925-3082/Domain: laminin G repeat homology <LG5>  
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:45,79,370,374,531,562,672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,1718,  
e (Asn) (covalent) #status predicted  
F:304-312/Disulfide bonds: #status experimental  
F:770,857,1999,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status experin  
F:845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent

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Query Match      8.8%; Score 125.5; DB 1; Length 3084;
Best Local Similarity 26.8%; Pred. No. 0.2;
Matches 51; Conservative 16; Mismatches 58; Indels 65; Gaps 14;

Qy 18 CEKVGAVQNSCDNCQP---GTFCKRY-----NPVCK--SCPPSPFSSIGGQPNIC--NIC 64
Db 813 CHLTGEEVVCDCQCAPGYSGWCERCADGYGNGPTVPGGTCVPC-----NCSGNVD 863

Qy 65 RVCAGYFRFKKFCSS-----THNAECE-CIEGFH---CLGPGQCTRCE----- 102
Db 864 PLEAGH-----CDSVTGECLKLWNTDGAHCERCADGFYGDVATKACRACDCHENGSL 917

Qy 103 -----KDCRPQOELTKQCKTCSLGTFTNDQNGTGVCRPWTNCSLDGRSVLKTGTT 152
Db 918 SGVCHLETGLCDCKP--HVTGQQCQCLSGYYGLDTGLG-CVP-CNCSVEG-SVSDNCTE 972

Qy 153 EKDVVCGPPV 162
Db 973 EGQCHCGPGV 982

RESULT 32
T42629
tenascin-X - bovine
N;Alternate names: flexilin
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42629
R;Eleftheriou, F.; Exposito, J.Y.; Garrone, R.; Lethias, C.
J. Biol. Chem. 272, 22866-22874, 1997
A;Title: Characterization of the bovine tenascin-X.
A;Reference number: Z22180; MUID:97426436; PMID:9278449
A;Accession: T42629
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-4135 <ELE>
A;Cross-references: EMBL:Y11915; NID:G2462978; PIDN:CAA72671.1; PID:G2462979
C;Genetics:
A;Gene: TN-X
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C;Keywords: extracellular matrix; glycoprotein; heptad repeat

Query Match      8.8%; Score 125; DB 2; Length 4135;
Best Local Similarity 21.9%; Pred. No. 0.27;
Matches 56; Conservative 29; Mismatches 95; Indels 76; Gaps 13;

Qy 18 CEKVGAVQNS---CDNCQPGTFCRKYNPVCKSCPPSPFSSIGGQPNIC-----NICRV----- 66
Db 624 CHRRGRCEGRCVCDSGYTGPSG-----ATRTCP-----ADCRGRGRCVQGVCHVGYSG 674

Qy 67 -----CAGYFRFKKFCSSSTHNAECEIEGFHCLGPQCT--RCEKDCRPGQELT 112
Db 675 EDCGQEEPPASACPGCGPRELCSA---GQCVCVEGFR--GPDCAITCPGDCR-GRGEC 728

Qy 113 KQCKTCSLGTFTNDQNG-----TGVCRPWTNC--SLDGRSVLKTGTTTEK 154
Db 729 REGSCVCDGYAGDCGERVPAIEGRMRHLEETTVTEWTRAPGNVDAYEIQFIPTTEG 788

Qy 155 DVVCGPPVVSFPSTTISVTPEGGPGHSLQVL-----TLFLALTSALLL 199
Db 789 ---ASPPPTARVPSSASAYDQRLAPQEQYQVTVRALRGTNWGPASKTITTMIDGPQDL 845

Qy 200 ALIFITLLFSLVKWIR 215
Db 846 RVAVTPTTLELNWLR 861

RESULT 33
MWTHUB1
laminin beta-1 chain precursor - human
N;Alternate names: laminin chain B1
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 19-Jan-2001

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C;Accession: S13547; A28483; A26994; S23566
R;Vuolteenaho, R.; Chow, L.T.; Tryggvason, K.
J. Biol. Chem. 265, 15611-15616, 1990
A;Title: Structure of the human laminin B1 chain gene.
A;Reference number: S13547; MUID:90368768; PMID:1975589
A;Accession: S13547
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1786 <VUO>
A;Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913
A;Note: the nucleotide sequence was submitted to GenBank, February 1991
R;Pikkarainen, T.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.; Pihlajaniemi, T.; Saras
J. Biol. Chem. 262, 10454-10462, 1987
A;Title: Human laminin B1 chain. A multidomain protein with gene (LAMB1) locus in the q22
A;Reference number: A28483; MUID:87280097; PMID:3611077
A;Accession: A28483
A;Molecule type: mRNA
A;Residues: 1-1786 <PIK>
A;Cross-references: GB:M61951; GB:J02778; NID:G186911; PIDN:AAA59486.1; PID:G186913
R;Jaye, M.; Modi, W.S.; Ricca, G.A.; Mudd, R.; Chiu, I.M.; O'Brien, S.J.; Drohan, W.N.
Am. J. Hum. Genet. 41, 605-615, 1987
A;Title: Isolation of a cDNA clone for the human laminin-B1 chain and its gene localization
A;Reference number: A26994; MUID:88021029; PMID:3661559
A;Accession: A26994
A;Molecule type: mRNA
A;Residues: 1276-1469, 'V', 1471-1695, 'G', 1697-1709 <JAY>
A;Cross-references: EMBL:M20206; NID:G186914; PIDN:AAA59487.1; PID:G186915
R;Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P
A;Title: Genes for the human laminin B1 and B2 chains.
A;Reference number: S23566
A;Accession: S23566
A;Molecule type: DNA
A;Residues: 762-1786 <VU2>
A;Note: mRNA was also sequenced
C;Genetics:
A;Gene: GDB:LAMB1
A;Cross-references: GDB:119357; OMIM:150240
A;Map position: 7q31.1-7q31.3
A;Introns: 13/1; 71/3; 117/1; 141/3; 204/3; 226/1; 293/3; 334/1; 397/1; 457/1; 494/3; 521
64/3; 1513/1; 1582/2; 1629/3; 1688/3; 1742/1
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-1786/Product: laminin beta-1 chain #status predicted <MAT>
F;22-270/Domain: VI <DOM6>
F;271-548/Domain: V <DOM5>
F;271-332/Domain: laminin-type EGF-like homology <LE01>
F;335-395/Domain: laminin-type EGF-like homology <LE02>
F;398-455/Domain: laminin-type EGF-like homology <LE03>
F;458-507/Domain: laminin-type EGF-like homology <LE04>
F;463-468/Region: cell adhesion #status predicted
F;510-540/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;549-774/Domain: IV <DOM4>
F;662-668/Region: cell adhesion #status predicted
F;773-818/Domain: laminin-type EGF-like homology <LE06>
F;775-1178/Domain: III <DOM3>
F;821-864/Domain: laminin-type EGF-like homology <LE07>
F;867-914/Domain: laminin-type EGF-like homology <LE08>
F;917-973/Domain: laminin-type EGF-like homology <LE09>
F;923-927/Region: cell adhesion #status predicted
F;950-954/Region: cell adhesion #status predicted
F;976-1025/Domain: laminin-type EGF-like homology <LE10>
F;1028-1081/Domain: laminin-type EGF-like homology <LE11>
F;1084-1129/Domain: laminin-type EGF-like homology <LE12>
F;1132-1176/Domain: laminin-type EGF-like homology <LE13>
F;1179-1397/Domain: II <DOM2>
F;1179-1397/Region: heptad repeats
F;1398-1430/Domain: alpha <ADP>
F;1431-1786/Domain: I <DOM1>

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F;18-269/Domain: VI <DOM6>  
F;270-516/Domain: V <DOM5>  
F;270-324/Domain: laminin-type EGF-like homology <LE1>  
F;327-394/Domain: laminin-type EGF-like homology <LE2>  
F;397-451/Domain: laminin-type EGF-like homology <LE3>  
F;454-500/Domain: laminin-type EGF-like homology <LE4>  
F;503-512/Domain: laminin-type EGF-like homology <LE5>  
F;517-708/Domain: IVb <DOM4B>  
F;709-1159/Domain: IIIB <DOM3B>  
F;709-739/Domain: laminin-type EGF-like homology #status atypical <LE6>  
F;742-788/Domain: laminin-type EGF-like homology <LE7>  
F;791-846/Domain: laminin-type EGF-like homology <LE8>  
F;849-899/Domain: laminin-type EGF-like homology <LE9>  
F;902-948/Domain: laminin-type EGF-like homology <LE10>  
F;951-995/Domain: laminin-type EGF-like homology <LE11>  
F;998-1041/Domain: laminin-type EGF-like homology <LE12>  
F;1044-1087/Domain: laminin-type EGF-like homology <LE13>  
F;1090-1109/Domain: laminin-type EGF-like homology <LE14>  
F;1111-1147/Domain: laminin-type EGF-like homology #status atypical <LE15>  
F;1150-1159/Domain: laminin-type EGF-like homology #status atypical <LE16>  
F;1160-1361/Domain: Iva <DOM4A>  
F;1362-1553/Domain: IIIa <DOM3A>  
F;1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>  
F;1403-1449/Domain: laminin-type EGF-like homology <LE18>  
F;1452-1506/Domain: laminin-type EGF-like homology <LE19>  
F;1509-1553/Domain: laminin-type EGF-like homology <LE20>  
F;1554-2125/Domain: I/II, heptad repeats <DOM2>  
F;2116-2120/Region: cell adhesion #status predicted  
F;2126-3075/Domain: G <DOMG>  
F;2142-2300/Domain: laminin G repeat homology <LG1>  
F;2329-2484/Domain: laminin G repeat homology <LG2>  
F;2510-2676/Domain: laminin G repeat homology <LG3>  
F;2534-2536/Region: cell attachment (R-G-D) motif  
F;2739-2888/Domain: laminin G repeat homology <LG4>  
F;2916-3073/Domain: laminin G repeat homology <LG5>  
F;38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1917,1920,1930,1931,1932,1933,1934,1935,1936,1937,1938,1939,1940,1941,1942,1943,1944,1945,1946,1947,1948,1949,1950,1951,1952,1953,1954,1955,1956,1957,1958,1959,1960,1961,1962,1963,1964,1965,1966,1967,1968,1969,1970,1971,1972,1973,1974,1975,1976,1977,1978,1979,1980,1981,1982,1983,1984,1985,1986,1987,1988,1989,1990,1991,1992,1993,1994,1995,1996,1997,1998,1999,2000,2001,2002,2003,2004,2005,2006,2007,2008,2009,2010,2011,2012,2013,2014,2015,2016,2017,2018,2019,2020,2021,2022,2023,2024,2025,2026,2027,2028,2029,2030,2031,2032,2033,2034,2035,2036,2037,2038,2039,2040,2041,2042,2043,2044,2045,2046,2047,2048,2049,2050,2051,2052,2053,2054,2055,2056,2057,2058,2059,2060,2061,2062,2063,2064,2065,2066,2067,2068,2069,2070,2071,2072,2073,2074,2075,2076,2077,2078,2079,2080,2081,2082,2083,2084,2085,2086,2087,2088,2089,2090,2091,2092,2093,2094,2095,2096,2097,2098,2099,2100,2101,2102,2103,2104,2105,2106,2107,2108,2109,2110,2111,2112,2113,2114,2115,2116,2117,2118,2119,2120,2121,2122,2123,2124,2125,2126,2127,2128,2129,2130,2131,2132,2133,2134,2135,2136,2137,2138,2139,2140,2141,2142,2143,2144,2145,2146,2147,2148,2149,2150,2151,2152,2153,2154,2155,2156,2157,2158,2159,2160,2161,2162,2163,2164,2165,2166,2167,2168,2169,2170,2171,2172,2173,2174,2175,2176,2177,2178,2179,2180,2181,2182,2183,2184,2185,2186,2187,2188,2189,2190,2191,2192,2193,2194,2195,2196,2197,2198,2199,2200,2201,2202,2203,2204,2205,2206,2207,2208,2209,2210,2211,2212,2213,2214,2215,2216,2217,2218,2219,2220,2221,2222,2223,2224,2225,2226,2227,2228,2229,2230,2231,2232,2233,2234,2235,2236,2237,2238,2239,2240,2241,2242,2243,2244,2245,2246,2247,2248,2249,2250,2251,2252,2253,2254,2255,2256,2257,2258,2259,2260,2261,2262,2263,2264,2265,2266,2267,2268,2269,2270,2271,2272,2273,2274,2275,2276,2277,2278,2279,2280,2281,2282,2283,2284,2285,2286,2287,2288,2289,2290,2291,2292,2293,2294,2295,2296,2297,2298,2299,2300,2301,2302,2303,2304,2305,2306,2307,2308,2309,2310,2311,2312,2313,2314,2315,2316,2317,2318,2319,2320,2321,2322,2323,2324,2325,2326,2327,2328,2329,2330,2331,2332,2333,2334,2335,2336,2337,2338,2339,2340,2341,2342,2343,2344,2345,2346,2347,2348,2349,2350,2351,2352,2353,2354,2355,2356,2357,2358,2359,2360,2361,2362,2363,2364,2365,2366,2367,2368,2369,2370,2371,2372,2373,2374,2375,2376,2377,2378,2379,2380,2381,2382,2383,2384,2385,2386,2387,2388,2389,2390,2391,2392,2393,2394,2395,2396,2397,2398,2399,2400,2401,2402,2403,2404,2405,2406,2407,2408,2409,2410,2411,2412,2413,2414,2415,2416,2417,2418,2419,2420,2421,2422,2423,2424,2425,2426,2427,2428,2429,2430,2431,2432,2433,2434,2435,2436,2437,2438,2439,2440,2441,2442,2443,2444,2445,2446,2447,2448,2449,2450,2451,2452,2453,2454,2455,2456,2457,2458,2459,2460,2461,2462,2463,2464,2465,2466,2467,2468,2469,2470,2471,2472,2473,2474,2475,2476,2477,2478,2479,2480,2481,2482,2483,2484,2485,2486,2487,2488,2489,2490,2491,2492,2493,2494,2495,2496,2497,2498,2499,2500,2501,2502,2503,2504,2505,2506,2507,2508,2509,2510,2511,2512,2513,2514,2515,2516,2517,2518,2519,2520,2521,2522,2523,2524,2525,2526,2527,2528,2529,2530,2531,2532,2533,2534,2535,2536,2537,2538,2539,2540,2541,2542,2543,2544,2545,2546,2547,2548,2549,2550,2551,2552,2553,2554,2555,2556,2557,2558,2559,2560,2561,2562,2563,2564,2565,2566,2567,2568,2569,2570,2571,2572,2573,2574,2575,2576,2577,2578,2579,2580,2581,2582,2583,2584,2585,2586,2587,2588,2589,2590,2591,2592,2593,2594,2595,2596,2597,2598,2599,2600,2601,2602,2603,2604,2605,2606,2607,2608,2609,2610,2611,2612,2613,2614,2615,2616,2617,2618,2619,2620,2621,2622,2623,2624,2625,2626,2627,2628,2629,2630,2631,2632,2633,2634,2635,2636,2637,2638,2639,2640,2641,2642,2643,2644,2645,2646,2647,2648,2649,2650,2651,2652,2653,2654,2655,2656,2657,2658,2659,2660,2661,2662,2663,2664,2665,2666,2667,2668,2669,2670,2671,2672,2673,2674,2675,2676,2677,2678,2679,2680,2681,2682,2683,2684,2685,2686,2687,2688,2689,2690,2691,2692,2693,2694,2695,2696,2697,2698,2699,2700,2701,2702,2703,2704,2705,2706,2707,2708,2709,2710,2711,2712,2713,2714,2715,2716,2717,2718,2719,2720,2721,2722,2723,2724,2725,2726,2727,2728,2729,2730,2731,2732,2733,2734,2735,2736,2737,2738,2739,2740,2741,2742,2743,2744,2745,2746,2747,2748,2749,2750,2751,2752,2753,2754,2755,2756,2757,2758,2759,2760,2761,2762,2763,2764,2765,2766,2767,2768,2769,2770,2771,2772,2773,2774,2775,2776,2777,2778,2779,2780,2781,2782,2783,2784,2785,2786,2787,2788,2789,2790,2791,2792,2793,2794,2795,2796,2797,2798,2799,2800,2801,2802,2803,2804,2805,2806,2807,2808,2809,2810,2811,2812,2813,2814,2815,2816,2817,2818,2819,2820,2821,2822,2823,2824,2825,2826,2827,2828,2829,2830,2831,2832,2833,2834,2835,2836,2837,2838,2839,2840,2841,2842,2843,2844,2845,2846,2847,2848,2849,2850,2851,2852,2853,2854,2855,2856,2857,2858,2859,2860,2861,2862,2863,2864,2865,2866,2867,2868,2869,2870,2871,2872,2873,2874,2875,2876,2877,2878,2879,2880,2881,2882,2883,2884,2885,2886,2887,2888,2889,2890,2891,2892,2893,2894,2895,2896,2897,2898,2899,2900,2901,2902,2903,2904,2905,2906,2907,2908,2909,291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A;Note: the nucleotide sequence was submitted to GenBank, February 1991  
R;Pikkarainen, T.; Kallunki, T.; Tryggvason, K.  
J. Biol. Chem. 263, 6751-6758, 1988  
A;Title: Human laminin B2 chain. Comparison of the complete amino acid sequence with the  
A;Reference number: A28158; MUID:88198245; PMID:3360804  
A;Accession: A28158  
A;Molecule type: mRNA  
A;Residues: 1-211, 'I', 213-1609 <PIK>  
A;Cross-references: EMBL:J03202; NID:gl86916; PIDN:AAA59488.1; PID:g307107  
R;Fukushima, Y.; Pikkarainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; He  
Cytogenet. Cell Genet. 48, 137-141, 1988  
A;Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene b  
A;Reference number: S13549; MUID:89169663; PMID:3234037  
A;Accession: S13549  
A;Molecule type: mRNA  
A;Residues: 1393-1609 <FUK>  
A;Cross-references: EMBL:M27654; NID:gl86923; PIDN:AAA59489.1; PID:g186924  
R;Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,  
Lab. Invest. 60, 772-782, 1989  
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha  
A;Reference number: A34961; MUID:89280632; PMID:2733383  
A;Accession: B34961  
A;Molecule type: mRNA  
A;Residues: 868-1551, 'N', 1553-1609 <OLS>  
R;Santos, C.L.S.; Sabbaga, J.; Brentani, R.  
DNA Seq. 1, 275-277, 1991  
A;Title: Differences in human laminin B2 sequences.  
A;Reference number: S14664; MUID:92216129; PMID:1806043  
A;Accession: S14664  
A;Molecule type: mRNA  
A;Residues: 1282-1609 <SAN>  
A;Cross-references: EMBL:X13939; NID:g34237; PIDN:CAA32122.1; PID:g34238  
R;Vuolteenaho, R.; Kallunki, T.; Chow, L.; Ikonen, J.; Pikkarainen, T.; Tryggvason, K.  
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 175-193, Academic P  
A;Title: Genes for the human laminin B1 and B2 chains.  
A;Reference number: S23566  
A;Accession: S23567  
A;Molecule type: DNA  
A;Residues: 801-1481, 'R', 1483-1609 <VUO>  
A;Note: mRNA was also sequenced  
C;Genetics:  
A;Gene: GDB:LAMC1; LAMB2  
A;Cross-references: GDB:120136; OMIM:150290  
A;Map position: 1q31-1q31  
A;Introns: 140/1; 241/3; 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/1;  
/3; 1525/1  
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin  
C;Function:  
A;Description: interact with cells and with other basement membrane proteins to promote  
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology  
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;34-1609/Product: laminin gamma-1 chain #status predicted <MAT>  
F;34-285/Domain: VI <DOM6>  
F;286-504/Domain: V <DOM5>  
F;286-339/Domain: laminin-type EGF-like homology <LE01>  
F;342-395/Domain: laminin-type EGF-like homology <LE02>  
F;398-442/Domain: laminin-type EGF-like homology <LE03>  
F;445-492/Domain: laminin-type EGF-like homology <LE04>  
F;495-504/Domain: laminin-type EGF-like homology #status atypical <LE05>  
F;505-689/Domain: IV <DOM4>  
F;690-1034/Domain: III <DOM3>  
F;690-721/Domain: laminin-type EGF-like homology #status atypical <LE06>  
F;724-770/Domain: laminin-type EGF-like homology <LE07>  
F;773-825/Domain: laminin-type EGF-like homology <LE08>  
F;828-881/Domain: laminin-type EGF-like homology <LE09>  
F;884-932/Domain: laminin-type EGF-like homology <LE10>  
F;935-980/Domain: laminin-type EGF-like homology <LE11>  
F;983-1028/Domain: laminin-type EGF-like homology <LE12>  
F;1035-1609/Domain: II/I <DOM1>  
F;1035-1609/Region: heptad repeats  
F;40-50/Disulfide bonds: #status predicted  
F;60,134,576,650,1022,1107,1161,1175,1205,1223,1241,1380,1395,1439/Binding site: carbonyl

F;1031,1034,1600/Disulfide bonds: interchain #status predicted

Query Match 8.6%; Score 122.5; DB 1; Length 1609;  
Best Local Similarity 24.2%; Pred. No. 0.2;  
Matches 54; Conservative 22; Mismatches 56; Indels 91; Gaps 17;

QY 18 CEKVG-----AVQNSCDNCQP-----GTFC-----RKYNPVCKSCPPSTFSSIGGQPNCN 62  
Db 751 CEKSDGYGDSTAGTSSDCQPCPGSSCAVVPKTKVVCTNCTGTGK-----RCE 805  
QY 63 ICRVCAGYF-----RFFKFSSTHN-----AEC-ECI---EGFHC--- 93  
Db 806 LCD--DGYFGDPLGRNGPVLRLCRLQCSNDIDPNVAGNCNRLTGECLKCIYNTAGFFCDR 863  
QY 94 -----LGP-----QCTRC-----EKDCRP--GQ-----ELTKQGCKTCSLGT 123  
Db 864 CKDGFNGPLAPNADKCKACNCNPNYGMKQSSCNPNVTGQCECLPHVTGDCGACDPGF 923  
QY 124 FNDQGTGVCRPWTNC-----SLDGRSVLKTGTTTEKDVVCGPPV 162  
Db 924 YNLQSGQGER--CDCHALGSTNGQCDIRTGQCE-----CQPGI 960

RESULT 39

T22759  
hypothetical protein F55H12.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Aug-2000  
C;Accession: T22759  
R;Dobson, R.  
submitted to the EMBL Data Library, October 1996  
A;Reference number: Z19610  
A;Accession: T22759  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2824 <WIL>  
A;Cross-references: EMBL:Z81091; PIDN:CAB03143.1; GSPDB:GN00019; CESP:F55H12.3  
A;Experimental source: clone F55H12  
C;Genetics:  
A;Gene: CESP:F55H12.3  
A;Map position: 1  
A;Introns: 87/1; 98/1; 126/2; 201/3; 343/3; 406/1; 576/3; 656/1; 825/3; 869/1; 909/1; 969/1;  
7/1; 1755/2; 1800/1; 1850/3; 1896/1; 2003/3; 2035/3; 2082/3; 2119/1; 2144/1; 2200/2; 2275/2;  
C;Superfamily: LDL receptor ligand-binding repeat homology  
F;243-279/Domain: LDL receptor ligand-binding repeat homology <LDL>

Query Match 8.6%; Score 122.5; DB 2; Length 2824;

Best Local Similarity 23.6%; Pred. No. 0.31;  
Matches 59; Conservative 31; Mismatches 113; Indels 47; Gaps 13;

QY 22 GAVQNS-C-DNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPNICRVCAGYRFRKFCSS 79  
Db 2470 GAVDESQCYVNCPIGQFESK--GLCNPCPEGTGPTTGLRKC-----ICCG-----FDLS 2517  
QY 80 THNAEC-ECIEG-----FHCLGPQCTRCCKDCRPGQELT-KQGCKTCSL 121  
Db 2518 TFGGPCIQCPRLTTSQASTSINSCDTINCIDAN-TMINKNVTGVPSTPYSEICIAEQ 2576  
QY 122 GTFNDQNGTGVCRPWTNCSLDGRSVLKT-GTEKDVV-----CGPPVVSFSPSTTISVT 174  
Db 2577 GTFQNVSNSDSCIPCSDLSENATSIPTVTCQSTCSDAIPTAGCNCQLQONGKSSMITRNC 2636  
QY 175 PEGGPGGHSLOVLTFLALTSALLLALIFITLLF---SVLKWIRK----KFPPIFKQPFK 227  
Db 2637 PEVTPVPGNSNAIKIVLGVVFGVLLIIIVLVLCPRKQIIAIFRKTDTSDNQHVLSHWD 2696  
QY 228 KTTGAAQEEED 237  
Db 2697 NATNRNEEN 2706

RESULT 40

T23433



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:56 ; Search time 20.1644 Seconds  
(without alignments)  
661.065 Million cell updates/sec

Title: US-10-067-122B-2

Perfect score: 1428

Sequence: 1 MGNNCYNVIVLLVGCCK.....DACSCRCQEEGGGGYEL 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	1428	100.0	256	1 TNR9_MOUSE	P20334 mus musculu
2	795	55.7	255	1 TNR9_HUMAN	Q07011 homo sapien
3	237	16.6	415	1 TNR3_MOUSE	P50284 mus musculu
4	215	15.1	625	1 TR11_MOUSE	O35305 mus musculu
5	208.5	14.6	277	1 TNR5_HUMAN	P25942 homo sapien
6	205.5	14.4	616	1 TR11_HUMAN	Q9Y6Q6 homo sapien
7	203.5	14.3	228	1 TR18_MOUSE	O35714 mus musculu
8	202.5	14.2	277	1 TNR4_HUMAN	P43489 homo sapien
9	202	14.1	435	1 TNR3_HUMAN	P36941 homo sapien
10	197	13.8	241	1 TR18_HUMAN	Q9Y5U5 homo sapien
11	197	13.8	461	1 TR1B_HUMAN	P20333 homo sapien
12	188	13.2	401	1 T11B_HUMAN	O00300 homo sapien
13	186.5	13.1	289	1 TNR5_MOUSE	P27512 mus musculu
14	185	13.0	300	1 TR6B_HUMAN	Q95407 homo sapien
15	185	13.0	474	1 TR1B_MOUSE	P25119 mus musculu
16	180.5	12.6	655	1 TR21_HUMAN	O75509 homo sapien
17	179	12.5	401	1 T11B_RAT	O08727 rattus norv
18	177	12.4	401	1 T11B_MOUSE	O08712 mus musculu
19	176.5	12.4	283	1 TR14_HUMAN	Q92356 homo sapien
20	170.5	11.9	271	1 TNR4_RAT	P15725 rattus norv
21	170	11.9	655	1 TR21_MOUSE	Q9epu5 mus musculu
22	169.5	11.9	250	1 TNR7_MOUSE	P41272 mus musculu
23	167	11.7	269	1 TNR5_BOVIN	Q28203 bos taurus
24	166.5	11.7	260	1 TNR7_HUMAN	P26842 homo sapien
25	158	11.1	272	1 TNR4_MOUSE	P47741 mus musculu
26	141.5	9.9	3695	1 LMA5_HUMAN	O15230 homo sapien
27	140.5	9.8	325	1 VT2_SFVKA	P25943 shope fibro
28	139.5	9.8	416	1 TR16_CHICK	P18519 gallus gall
29	138	9.7	349	1 CRMB_VARV	P34015 variola vir
30	138	9.7	3106	1 LMA2_MOUSE	Q60675 mus musculu
31	135.5	9.5	713	1 TSA4_GIALA	P21849 giardia lam
32	135.5	9.5	3110	1 LMA2_HUMAN	P24043 homo sapien
33	135	9.5	427	1 TR16_HUMAN	P08138 homo sapien

ALIGNMENTS

RESULT 1

TNR9\_MOUSE

ID	TNR9_MOUSE	STANDARD;	PRT;	256 AA.
AC	P20334;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB			
DE	ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).			
GN	TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89184547; PubMed=2784565;			
RA	Kwon B.S., Weissman S.M.;			
RT	"CDNA sequences of two inducible T-cell genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RX	MEDLINE=94179805; PubMed=8133039;			
RA	Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;			
RT	"Genomic organization and chromosomal localization of the T-cell			
RL	antigen 4-1BB.";			
RN	[3]			
RP	CHARACTERIZATION, AND SEQUENCE OF 25-29.			
RX	MEDLINE=93139510; PubMed=7678621;			
RA	Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.;			
RT	"Inducible T cell antigen 4-1BB. Analysis of expression and			
RL	function.";			
CC	J. Immunol. 150:771-781(1993).			
CC	-!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T			
CC	cell activation.			
CC	-!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.			
CC	ASSOCIATES WITH P56-LCK. Interacts with TRAF1, TRAF2 AND TRAF3 (By			
CC	similarity).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.			
CC	-!- INDUCTION: Optimal by PMA and ionomycin.			
CC	-!- SIMILARITY: Contains 4 TNFR-Cys repeats.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
CC	EMBL; J04492; AAA40167.1; -			
CC	EMBL; U02567; AAA93113.1; -			
DR				

DR PIR; B32393; B32393.  
 DR PDB; 1D0J; 26-SEP-01.  
 DR MGD; MGI:1101059; Tnfrsf9.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 1.  
 DR SMART; SM00208; TNFR; 2.  
 DR PROSITE; PS00552; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00550; TNFR\_NGFR\_2; FALSE NEG.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; 3D-structure.  
 FT SIGNAL 1 24  
 FT CHAIN 25 256  
 FT DOMAIN 25 187 TUMOR NECROSIS FACTOR RECEPTOR  
 FT TRANSMEM 188 208 SUPERFAMILY MEMBER 9.  
 FT DOMAIN 209 256 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 17 45 POTENTIAL.  
 FT REPEAT 46 85 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 86 117 TNFR-CYS 1.  
 FT REPEAT 118 159 TNFR-CYS 2.  
 FT REPEAT 118 159 TNFR-CYS 3.  
 FT REPEAT 118 159 TNFR-CYS 4.  
 FT DISULFID 28 37 BY SIMILARITY.  
 FT DISULFID 31 44 BY SIMILARITY.  
 FT DISULFID 47 61 BY SIMILARITY.  
 FT DISULFID 64 77 BY SIMILARITY.  
 FT DISULFID 67 85 BY SIMILARITY.  
 FT DISULFID 87 93 BY SIMILARITY.  
 FT DISULFID 98 105 BY SIMILARITY.  
 FT DISULFID 101 116 BY SIMILARITY.  
 FT DISULFID 119 133 BY SIMILARITY.  
 FT DISULFID 139 158 BY SIMILARITY.  
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 100.0%; Score 1428; DB 1; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 2e-110;  
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNVCYNVVVIVLLVGCCKVAVQNSCDNCQPGTFCKYKYNPVCKSCPPSTFFSIGGQPN 60  
 DB 1 MGNVCYNVVVIVLLVGCCKVAVQNSCDNCQPGTFCKYKYNPVCKSCPPSTFFSIGGQPN 60  
 QY 61 CNICRVACAGYFRFKFCSSTHNAECIEGFHCLGPOCTRCEKDCRPGQELTKQGCKTCS 120  
 DB 61 CNICRVACAGYFRFKFCSSTHNAECIEGFHCLGPOCTRCEKDCRPGQELTKQGCKTCS 120  
 QY 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTTEGGPG 180  
 DB 121 LGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSFSPSTTISVTTEGGPG 180  
 QY 181 GHSLOVTLFLALTSALLLALIFITLPSVLKWKIRKPPHIFKQPEKKTGAAQBEDACS 240  
 DB 181 GHSLOVTLFLALTSALLLALIFITLPSVLKWKIRKPPHIFKQPEKKTGAAQBEDACS 240  
 QY 241 CRCPQEEGGGGGYEL 256  
 DB 241 CRCPQEEGGGGGYEL 256

## RESULT 2

TNR9\_HUMAN  
 ID TNR9\_HUMAN STANDARD; PRT; 255 AA.  
 AC Q07011;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB  
 DE ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA  
 DE (CD137 antigen).  
 GN TNFRSF9 OR ILA OR CD137.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=94374434; PubMed=8088337;  
 RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,  
 RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;  
 RT "Molecular and biological characterization of human 4-1BB and its  
 RT ligand.";  
 RL Eur. J. Immunol. 24:2219-2227(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=94085794; PubMed=8262389;  
 RA Schwarz H., Tuckwell J., Lotz M.;  
 RT "A receptor induced by lymphocyte activation (ILA): a new member of  
 RT the human nerve-growth-factor/tumor-necrosis-factor receptor  
 RT family.";  
 RL Gene 134:295-298(1993).  
 RN [3]  
 RP REVISION TO 107.  
 RA Schwarz H.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=95347766; PubMed=7622190;  
 RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,  
 RA Kwon B.S.;  
 RT "Characterization of human homologue of 4-1BB and its ligand.";  
 RL Immunol. Lett. 45:67-73(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Pearce A.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=2388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP INTERACTION WITH TRAF1; TRAF2 AND TRAF3.  
 RX MEDLINE=98078711; PubMed=9418902;  
 RA Arch R.H., Thompson C.B.;  
 RT "4-1BB and Ox40 are members of a tumor necrosis factor (TNF)-nerve  
 RT growth factor receptor subfamily that bind TNF receptor-associated  
 RT factors and activate nuclear factor kappaB.";  
 RL Mol. Cell. Biol. 18:558-565(1998).  
 RN [8]  
 RP INTERACTION WITH TRAF1 AND TRAF2.  
 RX MEDLINE=98270914; PubMed=9607925;  
 RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,  
 RA Goldstein M.D., Bangia N., Desenedette M.A., Mak T.W., Choi Y.,  
 RA Watts T.H.;  
 RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by

RT 4-1BB ligand.;  
RL J. Exp. Med. 187:1849-1862(1998).  
RN [9]  
RP INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.  
RX MEDLINE=21662677; PubMed=11804328;  
RA Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;  
RT "A novel leucine-rich repeat protein (LRR-1): potential involvement in  
RL 4-1BB-mediated signal transduction.";  
RL Mol. Cells 12:304-312(2001).  
CC -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T  
CC cell activation.  
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with  
CC LRR-repeat protein 1/LRR-1.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U03397; AAA53133.1; -  
DR EMBL; L12964; AAA62478.2; -  
DR EMBL; AL009183; CAB57398.1; -  
DR EMBL; BC006196; AAA06196.1; -  
DR PIR; I38426; I38426.  
DR Genew; HGNC:11924; TNFRSF9.  
DR MIM; 602250; -  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0004872; F:receptor activity; TAS.  
DR GO; GO:0006917; P:induction of apoptosis; TAS.  
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.  
DR InterPro; IPR001368; TNFR\_C6.  
DR Pfam; PF00020; TNFR\_C6; 2.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00650; TNFR\_NGFR\_2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 255  
FT TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER 9.  
FT EXTRACELLULAR (POTENTIAL).  
FT POTENTIAL.  
FT TRANSMEM  
FT DOMAIN 18 186  
FT TRANSMEM 187 213  
FT DOMAIN 214 255  
FT CYTOPLASMIC (POTENTIAL).  
FT REPEAT 17 45  
FT TNFR-CYS 1.  
FT REPEAT 47 86  
FT TNFR-CYS 2.  
FT REPEAT 87 118  
FT TNFR-CYS 3.  
FT REPEAT 119 159  
FT TNFR-CYS 4.  
FT INTERACTS WITH LRR-1.  
FT DOMAIN 214 255  
FT DISULFID 28 37  
FT BY SIMILARITY.  
FT DISULFID 31 45  
FT BY SIMILARITY.  
FT DISULFID 48 62  
FT BY SIMILARITY.  
FT DISULFID 65 78  
FT BY SIMILARITY.  
FT DISULFID 68 86  
FT BY SIMILARITY.  
FT DISULFID 88 94  
FT BY SIMILARITY.  
FT DISULFID 99 106  
FT BY SIMILARITY.  
FT DISULFID 102 117  
FT BY SIMILARITY.  
FT DISULFID 121 133  
FT BY SIMILARITY.  
FT DISULFID 139 158  
FT BY SIMILARITY.  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 138 138  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 149 149  
FT SEQUENCE 255 AA; 27899 MW; F3A563FE5EF00460 CRC64;  
SQ

Query Match 55.7%; Score 795; DB 1; Length 255;  
Best Local Similarity 58.4%; Pred. No. 2e-58;  
Matches 149; Conservative 31; Mismatches 67; Indels 8; Gaps 6;

QY 1 MGNNCYNVVVIVLLVGVCEKVGAVQNSCDNCPQGTFC-RKYNPVCKSCPPSTSSIGGP 59  
Db 1 MGNSCYNIVATLLLVNFRTRSLQDPCSNCPAGTCDNNRNQICSPCPNSESAGQR 60  
QY 60 NCNIRVCAGYFRFKFCSSSTHNAECIEGFHCLGPQCTRCCKDCRPGQELTKGCKTC 119  
Db 61 TCDICRQCKGVFRTRKECSSTSNABCDCTPGFHCIGAGCSMCEQDCKQGLTKGCKDC 120  
QY 120 SLGTFNDQGTGVCPRWTNCSLDGRSVLKTGTTKDVVCGPPVVSFSPSTTISVTEGGP 179  
Db 121 CFGTFNDQK-RGICRPTNCSLDGKSVLVNGTKERDVVCGPSPADLSFGAS-SVTPP-AP 177  
QY 180 G---GHSLOVLTFLALTS-ALLLALIFITLLFSLVKWIRKFKPHFKQPKKTTGAQAE 235  
Db 178 AREPGHSPQIIISFFALTSTALLFLFLFTLRFSVVKRGRKLLYIFKQPFMRPVQTQE 237  
QY 236 EDACSCRCPEEEEGG 250  
Db 238 EDGSCRCPEEEEGG 252

## RESULT 3

TNR3\_MOUSE  
ID TNR3\_MOUSE STANDARD; PRT; 415 AA.  
AC P50284;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 3 precursor  
DE (Lymphotoxin-beta receptor).  
GN LTBR OR TNFRSF3 OR TNFR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CVB; TISSUE=Lung;  
RX MEDLINE=96072804; PubMed=7594541;  
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
RA Browning J.L., Ware C.F.;  
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
RT and expression."  
RL J. Immunol. 155:5280-5288(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96163885; PubMed=8586432;  
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,  
RA Honjo T.;  
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
RT sequence trap and chromosomal mapping."  
RL Genomics 30:312-319(1995).  
RN [3]  
RP INTERACTION WITH TRAF5.  
RC STRAIN=BALB/c;  
RX MEDLINE=96278943; PubMed=8663299;  
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,  
RA Yagita H., Okumura K.;  
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for  
RT the lymphotoxin-beta receptor."  
RL J. Biol. Chem. 271:14661-14664(1996).  
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3  
CC and TRAF5. May play a role in the development of lymphoid organs  
CC (By similarity).  
CC -!- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.  
CC Associates with TRAF3 and TRAF4 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its

















OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90260639; PubMed=2160731;  
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
RA Dower S.K., Cosman D., Goodwin R.G.;  
RT "A receptor for tumor necrosis factor defines an unusual family of  
RT cellular and viral proteins.";  
RL Science 248:1019-1023(1990).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANT ARG-196.  
RX MEDLINE=91045991; PubMed=2172983;  
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
RT "A second tumor necrosis factor receptor gene product can shed a  
RT naturally occurring tumor necrosis factor inhibitor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96299745; PubMed=8661109;  
RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,  
RA Brodeur G.M.;  
RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
RL Genomics 35:94-100(1996).  
RN [4]  
RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND  
RP ARG-301.  
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,  
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PNS;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP SEQUENCE OF 37-461 FROM N.A.  
RX MEDLINE=91370690; PubMed=1966549;  
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,  
RA Brockhaus M., Lesslauer W.;  
RT "Two human TNF receptors have similar extracellular, but distinct  
RT intracellular, domain sequences.";  
RL Cytokine 2:231-237(1990).  
RN [7]  
RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.  
RX MEDLINE=90349572; PubMed=2166946;  
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
RA Ringold G.M.;  
RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
RT and demonstration of a shed form of the receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
RN [8]  
RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.  
RX MEDLINE=21069356; PubMed=11197692;  
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;  
RT "New single nucleotide polymorphisms in the coding region of human  
RT TNFR2, association with systemic lupus erythematosus.";  
RL Genes Immun. 1:501-503(2000).  
RN [9]  
RP SEQUENCE OF 27-31.  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536(1990).  
RN [10]  
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
RX MEDLINE=91056048; PubMed=2173696;  
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
RA Brockhaus M.;  
RT "Purification and partial amino acid sequence analysis of two  
RT distinct tumor necrosis factor receptors from HL60 cells.";  
RL J. Biol. Chem. 265:20131-20138(1990).  
RN [11]  
RP CHARACTERIZATION.  
RX MEDLINE=93016040; PubMed=1328224;  
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
RA Lipari M.T., Goeddel D.V.;  
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
RT Characterization of ligand binding, internalization, and receptor  
RT phosphorylation.";  
RL J. Biol. Chem. 267:21172-21178(1992).  
RN [12]  
RP INTERACTION WITH TRAF2.  
RX MEDLINE=94349371; PubMed=8069916;  
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;  
RT "A novel family of putative signal transducers associated with the  
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";  
RL Cell 78:681-692(1994).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH  
RP TRAF2.  
RX MEDLINE=99221490; PubMed=10206649;  
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
RT "Structural basis for self-association and receptor recognition of  
RT human TRAF2.";  
RL Nature 398:533-538(1999).  
RN [14]  
RP VARIANTS ARG-196 AND LYS-232.  
RX MEDLINE=21603988; PubMed=11762942;  
RA Morita C., Horiuchi T., Tsukamoto H., Hatta N., Kikuchi Y.,  
RA Arinobu Y., Otsuka T., Sawabe T., Harashima S., Nagasawa K., Niho Y.;  
RT "Association of tumor necrosis factor receptor type II polymorphism  
RT 196R with systemic lupus erythematosus in the Japanese: molecular and  
RT functional analysis.";  
RL Arthritis Rheum. 44:2819-2827(2001).  
RN [15]  
RP VARIANT ARG-196.  
RX MEDLINE=22151311; PubMed=12161545;  
RA Peral B., San Millan J.L., Castello R., Moghetti P.,  
RA Escobar-Morreale H.F.;  
RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the  
RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic  
RT ovary syndrome and hyperandrogenism.";  
RL J. Clin. Endocrinol. Metab. 87:3977-3983(2002).  
CC -!- FUNCTION: Receptor with high affinity for homotrimeric  
CC approximately 5-fold lower affinity for homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the  
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. The TNF  
CC receptor 2 mediates most of the metabolic effects of TNF-alpha.  
CC -!- SUBUNIT: Binds to TRAF2.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC -!- PTM: Phosphorylated; mainly on serine residues and with a very low  
CC level on threonine residues.

CC -!- PTM: A soluble form (tumor necrosis factor binding protein 2) is  
CC produced from the membrane form by proteolytic processing.  
CC -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and  
CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid  
CC arthritis (RA). Enbrel consist of the extracellular ligand-binding  
CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to  
CC TNF-alpha and blocks its interactions with receptors.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".  
CC -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
CC WWW="http://www.enbrel.com/".  
CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; M32315; AAA59929.1; -.  
DR EMBL; U52165; AAC50622.1; -.  
DR EMBL; U52156; AAC50622.1; JOINED.  
DR EMBL; U52157; AAC50622.1; JOINED.  
DR EMBL; U52158; AAC50622.1; JOINED.  
DR EMBL; U52159; AAC50622.1; JOINED.  
DR EMBL; U52160; AAC50622.1; JOINED.  
DR EMBL; U52161; AAC50622.1; JOINED.  
DR EMBL; U52162; AAC50622.1; JOINED.  
DR EMBL; U52163; AAC50622.1; JOINED.  
DR EMBL; U52164; AAC50622.1; JOINED.  
DR EMBL; M55994; AAA36755.1; -.  
DR EMBL; AY264804; AAC89076.1; -.  
DR EMBL; AY342040; AAP88939.1; -.  
DR EMBL; BC052977; AAH52977.1; -.  
DR EMBL; S63368; AAB19824.2; -.  
DR EMBL; M35857; AAA63262.1; -.  
DR EMBL; AB030950; BAA89053.1; -.  
DR PIR; A35356; A35356.  
DR PDB; 1CA9; 12-APR-99.  
DR Genew; HGNC:11917; TNFRSF1B.

Query Match 13.8%; Score 197; DB 1; Length 461;  
Best Local Similarity 26.3%; Pred. No. 4.7e-09;  
Matches 72; Conservative 33; Mismatches 99; Indels 70; Gaps 15;  
QY 25 QNSCDNCQPG-----TFCKR-YNPVCKSCPPSTFSSI-GGQPNCNIC-RVCAGYFRFKKFC 77  
Db 51 QMCCSKCSPGQHAQVCTKTSTVCDSCEDSTYTQLWNVVECLSCGSRCSDDQVETQAC 110  
QY 78 SSTHNAECEIEGFHC-LGPO--CTRCE--KDCRPGQELTKQG-----CKTCSLGTG- 124  
Db 111 TREQNRICTRCGWYCALSKQEGRLCAPLEKCRPGFGVAPGTETSDVVCKPCAPGTES 170  
QY 125 NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC----- 158  
Db 171 NTTSSDTCRPHQICNV---VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQH 226  
QY 159 --GPPVVSFSPSTI-----SVTPGPGGHSLSQVLTFLALTSALLLALIFITLLFSV 210  
Db 227 TQTPPEPSTAPSTFLLPMGSPSPAEGSTGDFALPV-GLIVGVTALGLLIIGWNCV--I 283  
QY 211 LKWIRK-----KPPHIFKQPFKKTGAAQE 235  
Db 284 MTQVKKKPLCLQREAKVPHLPADKARGTQGPQEQ 317

RESULT 12  
T11B HUMAN  
ID T11B HUMAN STANDARD; PRT; 401 AA.  
AC O00300; O60236; Q9UHP4;  
DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 11B precursor  
DE (osteoprotegerin) (osteoclastogenesis inhibitory factor).  
GN TNFRSF11B OR OPG OR OCIF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=97262071; PubMed=9108485;  
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,  
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
RA Suggs S., Boyle W.J.;  
RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
RT of bone density";  
RL Cell 89:309-319(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung cancer;  
RX MEDLINE=98151033; PubMed=9492069;  
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,  
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,  
RA Tsuda E., Morinaga T., Higashio K.;  
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and  
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits  
RT osteoclastogenesis in vitro";  
RL Endocrinology 139:1329-1337(1998).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.  
RC TISSUE=Placenta;  
RX MEDLINE=98351569; PubMed=9688283;  
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;  
RT "Cloning and characterization of the gene encoding human  
RT osteoprotegerin/osteoclastogenesis-inhibitory factor";  
RL Eur. J. Biochem. 254:685-691(1998).  
RN [4]  
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 22-36 AND 378-401.  
RX MEDLINE=98238645; PubMed=9571159;  
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,  
RA Morinaga T., Tsuda E., Higashio K.;  
RT "Characterization of monomeric and homodimeric forms of  
RT osteoclastogenesis inhibitory factor";  
RL Biochem. Biophys. Res. Commun. 245:382-387(1998).



DE (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).

GN TNFRSF5 OR CD40.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM I).

RX MEDLINE=92105763; PubMed=1370315;

RA Torres R.M., Clark E.A.;

RT "Differential increase of an alternatively polyadenylated mRNA

RT species of murine CD40 upon B lymphocyte activation.";

RL J. Immunol. 148:620-626(1992).

RN [2]

RP REVISIONS.

RC STRAIN=BALB/c;

RA Torres R.M.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM I).

RC STRAIN=BALB/c; TISSUE=Liver;

RX MEDLINE=93094586; PubMed=1281194;

RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,

RA Howard M., Cockayne D.A.;

RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";

RL J. Immunol. 149:3921-3926(1992).

RN [4]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND

RP V).

RX MEDLINE=21117110; PubMed=11172023;

RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;

RT "Regulation of CD40 function by its isoforms generated through

RT alternative splicing.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

RN [5]

RP INTERACTION WITH TRAF3.

RX MEDLINE=95184010; PubMed=7533327;

RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;

RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";

RL Science 267:1494-1498(1995).

RN [6]

RP INTERACTION WITH TRAF5.

RX MEDLINE=96382484; PubMed=8790348;

RA Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,

RA Yamamoto T., Inoue J.-I.;

RT "TRAF5, a novel tumor necrosis factor receptor-associated factor

RT family protein, mediates CD40 signaling.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).

CC -I- FUNCTION: Receptor for TNFSF5/CD40L.

CC -I- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,

CC TRAF2 AND TRAF6 (By similarity).

CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV

CC and V); secreted (isoform II).

CC -I- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=5;

CC Name=I;

CC IsoId=P27512-1; Sequence=Displayed;

CC Name=II;

CC IsoId=P27512-2; Sequence=VSP\_006474, VSP\_006475;

CC Name=III;

CC IsoId=P27512-3; Sequence=VSP\_006477, VSP\_006478;

CC Name=IV;

CC IsoId=P27512-4; Sequence=VSP\_006479, VSP\_006480;

CC Name=V;

CC IsoId=P27512-5; Sequence=VSP\_006476;

CC -I- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -----

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CC -----

DR EMBL; M83312; AAB08705.1; -

DR EMBL; M94126; AAA37404.1; -

DR EMBL; M94129; AAA37404.1; JOINED.

DR EMBL; M94128; AAA37404.1; JOINED.

DR EMBL; M94127; AAA37404.1; JOINED.

DR EMBL; AJ401387; CAC29427.1; -

DR EMBL; AJ401388; CAC29428.1; -

DR EMBL; AJ401389; CAC29429.1; -

DR EMBL; AJ401390; CAC29430.1; -

DR PIR; A46476; A46476.

DR HSSP; P25942; 1CDF.

DR MGI; 88336; Tnf5.

DR InterPro; IPR008063; Fas\_receptor.

DR InterPro; IPR001368; TNFR\_C6.

DR Pfam; PF00020; TNFR\_C6; 4.

DR PRINTS; PR01580; FASRECEPTOR.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.

DR PROSITE; PS00500; TNFR\_NGFR\_2; 4.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;

KW Alternative splicing.

FT SIGNAL 1 19

FT CHAIN 20 289

FT DOMAIN 20 193

FT TRANSMEM 194 215

FT DOMAIN 216 289

FT REPEAT 25 60

FT REPEAT 61 103

FT REPEAT 104 144

FT REPEAT 145 187

FT DISULFID 26 37

FT DISULFID 38 51

FT DISULFID 41 59

FT DISULFID 62 77

FT DISULFID 83 103

FT DISULFID 105 119

FT DISULFID 111 116

FT DISULFID 125 143

FT CARBOHYD 153 153

FT VARSPLIC 166 203

FT VARSPLIC 204 289

FT VARSPLIC 187 216

FT VARSPLIC 216 234

FT VARSPLIC 235 289

FT VARSPLIC 216 222

FT VARSPLIC 223 289

FT SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

SQ

Query Match 13.1%; Score 186.5; DB 1; Length 289;

Best Local Similarity 25.1%; Pred. No. 2.2e-08;

Matches 61; Conservative 34; Mismatches 87; Indels 61; Gaps 11;

QY 28 CDNCQPGTFCRKY-----NPVCKSCPSTFSSIGGP-NCNICRVCAGY--FRFKKFCSS 79

DB 38 CDLCQPGSRLTSHCTALEKTCQPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGTA 97

QY 80 THNAECEIEGFHCLGPQCTRCCK--DCRPG-----QELTKQGCKTCSLGTNDQNGT 130

DB 98 ESDTVCTCKEGQHCCTSKDCEACAQHTPCIPFGVGMENATETTDVCHPCVPVGFSSNSSL 157

QY 131 -GVCPRWNCSLDGRSVLTKGTTEKDVVCGPPVVSFSPSTTISVTPGGGSHSLQVLT 189  
Db 158 FEKCPWTSCEDKNLEVLKGTSTQNTVICG-----L 188  
QY 190 FLALTSALLALI--FITLLFVLKWKIRKFFPHFKOP--FKKTTGAAQEEADACSCRCPO 245  
Db 189 KSRMRALLVPPVMGILITIFGVFLYIKK---VVKPKDNEMLPAPARRQD-----PQ 238  
QY 246 EEE 248  
Db 239 EME 241

RESULT 14

TR6B\_HUMAN STANDARD; PRT; 300 AA.  
AC 095407;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy  
GN TNFRSF6B OR DCR3 OR TR6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal lung;  
RX MEDLINE=99087326; PubMed=9872321;  
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,  
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,  
RA Goddard P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,  
RA Goddard A.D., Botstein D., Ashkenazi A.;  
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and  
RT colon cancer."  
RL Nature 396:699-703(1998).  
RN [2]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.  
RC TISSUE=Prostate;  
RX MEDLINE=99253915; PubMed=10318773;  
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;  
RT "A newly identified member of tumor necrosis factor receptor  
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis."  
RL J. Biol. Chem. 274:13733-13736(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=20122600; PubMed=10655513;  
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,  
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;  
RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors  
RT independent of gene amplification and its location in a four-gene  
RT cluster."  
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC Matthews L.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung, and Skin;  
RX MEDLINE=2238257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT  
CC and TNFSF6/FasL. Protects against apoptosis.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.  
CC Detected in adult stomach, spinal cord, lymph node, trachea,  
CC spleen, colon and lung. Highly expressed in several primary tumors  
CC from colon, stomach, rectum, esophagus and in SW480 colon  
CC carcinoma cells.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL; AF104419; AAD03056.1; -  
CC EMBL; AF134240; AAD29688.1; -  
CC EMBL; AF217796; AAF35244.1; -  
CC EMBL; AF217793; AAF33685.1; -  
CC EMBL; AF217794; AAF33686.1; -  
CC EMBL; AL121845; CAC03668.1; -  
CC EMBL; BC017065; AAH17065.1; -  
CC EMBL; BC034349; AAH34349.1; -  
CC HSP; O14763; IDOG.  
CC Genew; HGNC:11921; TNFRSF6B.  
CC MIM; 603361; -  
CC GO; GO:0005625; C:soluble fraction; TAS.  
CC GO; GO:0008189; F:apoptosis inhibitor activity; TAS.  
CC GO; GO:0004872; F:receptor activity; TAS.  
CC GO; GO:0006916; P:anti-apoptosis; TAS.  
CC InterPro; IPR001368; TNFR\_c6.  
CC Pfam; PF00020; TNFR\_c6; 4.  
CC SMART; SM00208; TNFR; 4.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
CC PROSITE; PS00650; TNFR\_NGFR\_2; 2.  
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 29  
FT CHAIN 30 300 TUMOR NECROSIS FACTOR RECEPTOR  
FT REPEAT 31 70 SUPERFAMILY MEMBER 6B.  
FT REPEAT 72 113 TNFR-CYS 1.  
FT REPEAT 115 150 TNFR-CYS 2.  
FT REPEAT 152 193 TNFR-CYS 3.  
FT DISULFID 49 62 TNFR-CYS 4.  
FT DISULFID 52 70 BY SIMILARITY.  
FT DISULFID 73 88 BY SIMILARITY.  
FT DISULFID 91 105 BY SIMILARITY.  
FT DISULFID 95 113 BY SIMILARITY.  
FT DISULFID 115 126 BY SIMILARITY.  
FT DISULFID 132 150 BY SIMILARITY.  
FT DISULFID 153 168 BY SIMILARITY.  
FT DISULFID 174 193 BY SIMILARITY.  
FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;

Query Match 13.0%; Score 185; DB 1; Length 300;  
Best Local Similarity 28.3%; Pred. No. 3e-08;  
Matches 65; Conservative 24; Mismatches 85; Indels 56; Gaps 14;

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CC -----

CC EMBL; M60469; AAA39752.1; -

DR EMBL; M59378; AAA40463.1; -

DR EMBL; U39488; AAA85021.1; -

DR EMBL; X87128; CAA60618.1; -

DR PIR; B38634; B38634.

DR HSSP; P19438; 1NCF.

DR MGD; MGI:1314883; Tnfrsflb.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.

DR GO; GO:0006954; P:inflammatory response; IMP.

DR GO; GO:0008220; P:necrosis; IMP.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 4.

DR SMART; SMO0208; TNFR; 4.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22

FT CHAIN 23 474

FT DOMAIN 23 258

FT TRANSMEM 259 288

FT DOMAIN 289 474

FT REPEAT 39 77

FT REPEAT 78 119

FT REPEAT 120 164

FT REPEAT 165 203

FT DISULFID 40 54

FT DISULFID 55 68

FT DISULFID 58 76

FT DISULFID 79 94

FT DISULFID 97 111

FT DISULFID 101 119

FT DISULFID 121 127

FT DISULFID 136 145

FT DISULFID 139 163

FT DISULFID 166 181

FT CARBOHYD 69 69

FT CARBOHYD 195 195

FT SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Qy Query Match 13.0%; Score 185; DB 1; Length 474;

Db Best Local Similarity 26.0%; Pred. No. 4.7e-08;

Qy 25 QNSCDNCQPGT----FCRK-YNPVCKSCPPSTFFSIGGQPNICRVCAGYFRFK----K 75

Db 52 QMCCAKCPGQYVHKFKNTSDTVCADCEASMTQVWNQ--FRCLSCSSCTTDOVEIR 109

Qy 76 FCSSTHNAECEIEGFHCL-----GPQTRCEKDCRPQELTKQG-----CKTCSL 121

Db 110 ACTKQNRVCAACEAGRYCALKTHSGSCRCQMLSK-CGPGFGVASSRAPNGNVLCACAP 168

Qy 122 GTFND-QNGTGVCPRWTNCSLDGRSVLTKTGTTEKDVVCGP--PVVSFSPSTTISVTP--- 175

Db 169 GTFSDTTSSTDVCRPHRICSI----LAIPGNASTDAVCAPESTLSAIPRTLYVSQPEPT 224

Qy 176 -----EGGP-----GGHSLQVLTFLALTSALLLALIFITLL 207

Db 225 RSQPLDQEPGPSQTPSILTSLSGTPTEQSTKGGISLPI-GLIVGVTS---LGLMLGLV 280

Qy 208 FSVLKWIRKKFPHIFKQPFKTTGAQEEEDACSCRPQEEEGGGGGE 255

Db 281 NCIIIVQKKKP-----SCLQDAKVPHPVDEKSDQDAVGLE 316

RESULT 16

TR21 HUMAN

ID TR21\_HUMAN STANDARD; PRT; 655 AA.

AC O75509; Q96D86;

DT 28-FEB-2003 (Rel. 41, Created)

Qy 28 CDNCQPGTF----CRKYNP-VCKSCPSTFFSIGGQ-PNCNICRV-CAGYFRFKFCSST 80

Db 49 CAQCPGTFVQPCRRDSPTTCGCPRRHYTQFWNLYLRCRYCNVLCGEREEARACHAT 108

Qy 81 HNAECEIEGFHCLGPQCTRCCKDPCPGQELTKQG-----CKTCSLGTFN-DQNGTGV 132

Db 109 HNRACRGTGFFAHAGFCL-E-HASCPCGAGVIAPGTPSQNTQCQCPGPTFSASSSSEQ 167

Qy 133 CRPWTNCSLDGRSVLTKTGTTEKDVVC-----GPP-----VVSFSPSTISV- 173

Db 168 CQPHRNCTALGLALNVGSSSHDTLCTGTFPLSTRVPGAEECERAVIDFVAFQDISIK 227

Qy 174 -----TPEG-GP-----GGHSLQV-----LTLFL-ALTSALLALI 202

Db 228 RLQRLQLALEAPEGWGTPPRAGRAALQLKRLRRRLTELLGAQDQALLVRL 277

RESULT 15

TR1B MOUSE

ID TR1B\_MOUSE STANDARD; PRT; 474 AA.

AC P25119; P97893;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (TNF-R2) (p75).

DE TNFRSF1B OR TNFR2 OR TNFR-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91187885; PubMed=1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.;

RA "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific."

RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91246168; PubMed=1645445;

RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;

RA "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."

RT Mol. Cell. Biol. 11:3020-3026 (1991).

RN [3]

RP SEQUENCE OF 1-26 FROM N.A.

RC STRAIN=NOD;

RA Jacob C.O., Liu J.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE OF 1-22 FROM N.A.

RC TISSUE=Liver;

RA Kissnerghis M., Fellows R., Feldmann M., Chernajovsky Y.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and approximately 5-fold lower affinity for homotrimeric TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By similarity).

CC -!- SUBUNIT: Binds to TRAF2 (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -----

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [6]  
RP INTERACTION WITH TRAF2 AND TRAF5.  
RX MEDLINE=97298041; PubMed=9153189;  
RA Hsu H., Solovjev I., Colombero A., Elliott R., Kelley M., Boyle W.J.;  
RT "ATAR, a novel tumor necrosis factor receptor family member, signals  
RT through TRAF2 and TRAF5.";  
RL J. Biol. Chem. 272:13471-13474 (1997).  
RN [7]  
RP INTERACTION WITH TRAF3 AND TRAF5.  
RX MEDLINE=97306297; PubMed=9162022;  
RA Marsters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,  
RA Ashkenazi A.;  
RT "Herpesvirus entry mediator, a member of the tumor necrosis factor  
RT receptor (TNFR) family, interacts with members of the TNFR-associated  
RT factor family and activates the transcription factors NF-kappaB and  
RT AP-1.";  
RL J. Biol. Chem. 272:14029-14032 (1997).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.  
RX MEDLINE=21403268; PubMed=11511370;  
RA Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,  
RA Eisenberg R.J., Wiley D.C.;  
RT "Herpes simplex virus glycoprotein D bound to the human receptor  
RT HveA.";  
RL Mol. Cell 8:169-179 (2001).  
CC -!- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays  
CC an important role in HSV pathogenesis because it enhanced the  
CC entry of several wildtype HSV strains of both serotypes into CHO  
CC cells, and mediated HSV entry into activated human T cells.  
CC -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION  
CC IN LUNG, SPLEEN, AND THYMUS.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -----  
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CC -----  
DR EMBL; U70321; AAB58354.1; -.  
DR EMBL; U81232; AAD00505.1; -.  
DR EMBL; AF153978; AAF75588.1; -.  
DR EMBL; AF373877; AAL47717.1; -.  
DR EMBL; AF373878; AAL47718.1; -.  
DR EMBL; BC002794; AAH02794.1; -.  
DR PDB; 1JMA; 26-SEP-01.  
DR Genew; HGNC:11912; TNFSF14.  
DR MIM; 602746; -.  
DR GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.  
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.  
DR GO; GO:0006955; P:immune response; TAS.  
DR InterPro; IPR008063; Fas receptor.  
DR InterPro; IPR001368; TNFR c6.  
DR Pfam; PF00020; TNFR c6; 3.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;  
KW 3D-structure.  
FT SIGNAL 1 38 POTENTIAL.

FT CHAIN 39 283 TUMOR NECROSIS FACTOR RECEPTOR  
FT DOMAIN 39 202 SUPERFAMILY MEMBER 14.  
FT TRANSMEM 203 223 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 224 283 POTENTIAL.  
FT REPEAT 42 75 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 78 119 TNFR-CYS 1.  
FT REPEAT 121 162 TNFR-CYS 2.  
FT DISULFID 42 53 TNFR-CYS 3.  
FT DISULFID 54 67  
FT DISULFID 57 75  
FT DISULFID 78 93  
FT DISULFID 96 111  
FT DISULFID 99 119  
FT DISULFID 121 138  
FT DISULFID 127 135  
FT CARBOHYD 110 110  
FT CARBOHYD 173 173  
FT VARIANT 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARIANT 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARIANT 241 241 K -> R (in dbSNP:4870).  
FT VARIANT 241 241 /FTId=VAR\_013007.  
FT VARIANT 241 241 V -> I.  
FT VARIANT 241 241 /FTId=VAR\_013440.  
FT TURN 44 45  
FT STRAND 46 46  
FT STRAND 49 49  
FT TURN 50 51  
FT STRAND 52 52  
FT STRAND 55 55  
FT STRAND 57 57  
FT TURN 59 60  
FT STRAND 61 65  
FT STRAND 74 77  
FT TURN 80 81  
FT STRAND 82 83  
FT STRAND 88 88  
FT STRAND 94 95  
FT TURN 101 104  
FT STRAND 105 109  
FT STRAND 118 121  
FT TURN 123 124  
FT STRAND 125 129  
FT STRAND 137 140  
SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;  
Query Match 12.4%; Score 176.5; DB 1; Length 283;  
Best Local Similarity 29.9%; Pred. No. 1.4e-07;  
Matches 49; Conservative 18; Mismatches 66; Indels 31; Gaps 9;  
Qy 1 MGNNCYNVVIVLLVGEK-----VGAVQNSCDNQPGTFCRK-----YNPVCKSPSPST 51  
Db 30 LGAPCY-----APALPSCKEDEVVPGS--ECCPKSPGYRVKEACGELTGTVCPCPPGT 82  
Qy 52 F-SSIGGQPNICRVG--AGYFRFKFKCSSTHNAECIEGFHCL---GPQCTRCB--K 103  
Db 83 YIAHLNGLSKLQCMQCDPAMGLRASRNCSTENAVGCGSPGHFCIVQDGDHCAACRAYA 142  
Qy 104 DCRPGQELTKQG-----CKTCSLGTFTNDQNGIGVCRPWTNCS 140  
Db 143 TSSPGQVRVQKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTCS 186  
RESULT 20  
TNFR4\_RAT  
ID TNFR4\_RAT STANDARD; PRT; 271 AA.  
AC P15725;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L  
DE receptor) (OX40 antigen) (MRC OX40).  
GN TNFRSF4 OR TXGPIL OR OX40.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



CC T-cells, B-cells and monocytes. In T-cells expression is highest  
CC in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- CAUTION: It is uncertain whether Met-1 or Met-25 is the initiator.  
CC -----  
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CC -----  
DR EMBL; AF322069; AAG38115.1; -;  
DR EMBL; AY043489; AAK74193.1; -;  
DR EMBL; BC016420; AAH16420.1; -;  
DR HSSP; O14763; 1D0G.  
DR MGD; MGI:2151075; Tnfrsf21.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 1.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS50017; DEATH DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 41  
FT CHAIN 42 655  
FT FT  
FT FT  
FT DOMAIN 42 349  
FT TRANSMEM 350 370  
FT DOMAIN 371 655  
FT DOMAIN 415 498  
FT REPEAT 50 88  
FT REPEAT 90 131  
FT REPEAT 133 167  
FT REPEAT 170 211  
FT DISULFID 67 80  
FT DISULFID 70 88  
FT DISULFID 91 106  
FT DISULFID 109 123  
FT DISULFID 113 131  
FT DISULFID 133 144  
FT DISULFID 150 168  
FT DISULFID 171 186  
FT DISULFID 192 211  
FT CARBOHYD 82 82  
FT CARBOHYD 141 141  
FT CARBOHYD 252 252  
FT CARBOHYD 257 257  
FT CARBOHYD 278 278  
FT CARBOHYD 289 289  
FT CONFLICT 352 352  
FT CONFLICT 523 523  
SQ SEQUENCE 655 AA; 71982 MW; 5EC7C51C7C99EFF7 CRC64;  
  
Query Match 11.9%; Score 170; DB 1; Length 655;  
Best Local Similarity 29.3%; Pred. No. 1.1e-06;  
Matches 55; Conservative 23; Mismatches 70; Indels 40; Gaps 10;  
  
QY 27 SCDCNCPGTFCKYNP-----VKSCPPSTFS-SIGQPNCNIC-RVCAGYFRFKFCSS 79  
DB 66 TCDKCPAGTYVSEHCTNMSLRVCSGPCAGTFRHENGIERCHDCSQPCPWPMIERLPCAA 125  
QY 80 THNAECECIEGFHCLGPQCTRCBKDCRPGQELTKQG-----CKTCSLGTFTND-QNGTG 131  
DB 126 LTRDECICPPGMYSQNGTTCAP-HTVCPVGVGVRKKGTEDEVRCCKQARGTFSDVPSSVM 184  
QY 132 VCRPWTNCSLDGRSVLKTGTTTRKDVVCG-----PP---VVSFS-----PST 169

Db 185 KCAHTDCLGQNLVVKPGTKETDNCVGMRLFFSSTNPPSSGTVTFSHPEHESHDPSS 244  
QY 170 TISVTPEG 177  
Db 245 TYE--PQG 250  
  
RESULT 22  
TNFR7\_MOUSE  
ID TNFR7\_MOUSE STANDARD; PRT; 250 AA.  
AC P41272;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, last annotation update)  
DE Tumor necrosis factor receptor superfamily member 7 precursor (CD27L  
DE receptor) (T-cell activation antigen CD27).  
GN TNFRSF7 OR CD27.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
RX MEDLINE=93209296; PubMed=8384562;  
RA Gravestein L.A., Blom B., Noltan L.A., de Vries E., van der Horst G.,  
RA Ossendorp F., Borst J., Loenen W.A.;  
RT "Cloning and expression of murine CD27: comparison with 4-1BB,  
RT another lymphocyte-specific member of the nerve growth factor  
RT receptor family";  
RL Eur. J. Immunol. 23:943-950(1993).  
CC -!- FUNCTION: Receptor for TNFSF7/CD27L. May play a role in survival  
CC of activated T-cells. May play a role in apoptosis through  
CC association with SIVA.  
CC -!- SUBUNIT: Homodimer. Interacts with SIVA and TRAF2 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: In thymus and spleen, but not in non-lymphoid  
CC tissues.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; L24495; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A49053; A49053.  
DR HSSP; P19438; INCF.  
DR MGD; MGI:88326; Tnfrsf7.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR InterPro; IPR008063; Fas receptor.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
KW Apoptosis; Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
FT SIGNAL 1 20  
FT CHAIN 21 250  
FT FT  
FT FT  
FT DOMAIN 21 182  
FT TRANSMEM 183 203  
FT DOMAIN 204 250  
FT REPEAT 26 63  
FT REPEAT 64 104  
FT REPEAT 105 141  
FT DISULFID 27 39  
FT DISULFID 40 53  
FT DISULFID 43 62



RA Loenen W.A., Graveststein L.A., Beumer S., Melief C.J., Hagemeijer A.,  
RA Borst J.,  
RA "Genomic organization and chromosomal localization of the human CD27  
RT gene";  
RL J. Immunol. 149:3937-3943 (1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.F., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [4]  
RP INTERACTION WITH TRAF2.  
RX MEDLINE=98355639; PubMed=9692890;  
RA Graveststein L.A., Amsen D., Boes M., Calvo C.R., Kruisbeek A.M.,  
RA Borst J.;  
RT "The TNF receptor family member CD27 signals to Jun N-terminal kinase  
RT via Traf-2";  
RL Eur. J. Immunol. 28:2208-2216 (1998).  
RN [5]  
RP INTERACTION WITH SIVA.  
RC TISSUE=Cervical carcinoma, and Thymus;  
RX MEDLINE=97322375; PubMed=9177220;  
RA Prasad K.V.S., Ao Z., Yoon Y., Wu M.X., Rizk M., Jacquot S.,  
RA Schlossman S.F.;  
RT "CD27, a member of the tumor necrosis factor receptor family, induces  
RT apoptosis and binds to Siva, a proapoptotic protein";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:6346-6351 (1997).  
CC -!- FUNCTION: Receptor for TNFSF7/CD27L. May play a role in survival  
CC of activated T-cells. May play a role in apoptosis through  
CC association with SIVA.  
CC -!- SUBUNIT: Homodimer. Interacts with SIVA and TRAF2.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Found in most T lymphocytes.  
CC -!- PTM: Phosphorylated and O-glycosylated (Probable).  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD27 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd27.htm".  
CC -----  
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CC -----  
DR EMBL; M63928; AAA58411.1; --  
DR EMBL; BC012160; AAA12160.1; --  
DR PIR; A46517; A46517.  
DR HSSP; P19438; INCF.  
DR Genew; HGNC:11922; TNFSF7.  
DR MIM; 186711; --  
DR GO; GO:0005886; C:plasma membrane; TAS.  
DR InterPro; IPR008063; Fas\_receptor.

DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR PRINTS; PRO1680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
KW Apoptosis; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
KW Phosphorylation; Polymorphism.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 260 TUMOR NECROSIS FACTOR RECEPTOR  
FT DOMAIN 21 191 SUPERFAMILY MEMBER 7.  
FT TRANSMEM 192 212 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 213 260 POTENTIAL.  
FT REPEAT 26 63 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 64 104 TNFR-CYS 1.  
FT REPEAT 105 141 TNFR-CYS 2.  
FT DISULFID 27 39 TNFR-CYS 3.  
FT DISULFID 40 53 BY SIMILARITY.  
FT DISULFID 43 62 BY SIMILARITY.  
FT DISULFID 65 81 BY SIMILARITY.  
FT DISULFID 84 96 BY SIMILARITY.  
FT DISULFID 87 104 BY SIMILARITY.  
FT DISULFID 106 117 BY SIMILARITY.  
FT DISULFID 112 120 BY SIMILARITY.  
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).  
FT MOD\_RES 219 219 PHOSPHORYLATION (POTENTIAL).  
FT VARIANT 59 59 A -> T (in dbSNP:758738).  
FT /FTid=VAR\_016148.  
SQ SEQUENCE 260 AA; 29156 MW; 43C38B92FA90D4E2 CRC64;  
Query Match 11.7%; Score 166.5; DB 1; Length 260;  
Best Local Similarity 25.0%; Pred No. 8.5e-07;  
Matches 63; Conservative 25; Mismatches 85; Indels 79; Gaps 12;  
Qy 28 CDNCQPGTF---CRKYNPV--CKSCPPS-TFS-SIGGQPNICRVACAGYFRKKFCSS 79  
Db 40 QMCCEPGTFLVKDCDQHRKAAQCDCIPGVSFSDHTRPHCESCRHCNSGLLVN-CTI 98  
Qy 80 THNAECECIEGFHCLGPQCTRCEDCRPGQELTKQGCKTCSLGTENDQNGTGVCRPWTNC 139  
Db 99 TANAEACRNGWQCRDKECTCD-----PLPNP 126  
Qy 140 SLDRSVLKTGTTTEKDVVCGPPVVSFSPSTT-----ISVTEGGPGHSLQVLTFLAL-- 193  
Db 127 SLTARS-----SQALSPHPQPTLHPVSEMLEARAGH-MQTLADFRQLPA 171  
Qy 194 -----TSALLLALIFITLLFSLVKWIRKFFPHIFKQPFKTTGAAQEDAC 239  
Db 172 RTLSTHWPPQSRSLCSDFIRILVIFSGMFLVFTLAGALFLH-QRRKYSRNKGESPVPEAE 230  
Qy 240 SCR--CPQEEEG 249  
Db 231 PCRYSCPREEEG 242  
RESULT 25  
TNFR4\_MOUSE  
ID TNR4\_MOUSE STANDARD; PRT; 272 AA.  
AC P47741;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L  
DE receptor) (OX40 antigen).  
GN TNFRSF4 OR TXGP1 OR OX40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;





Db 2043 KAGVTGRRCDRCQEGHF-----GFNGCGGCRPCA-----CGP 2074

Qy 78 ----SSTH--NAECECEIEGFHCLGPQCTRCCKDCRPGQ-ELTKQCKTCSLGTFTNDQNGT 130

Db 2075 AAESECHPQSGQCHCRPG--TMGPQC-----RECAPGYWGLPEQGCRRC-----QCPG 2121

Qy 131 GVCPRWT---NCSLDGRSVLKTGTTEKDWCGPPVVSFSPSTTIS-----VTPEGGPGGHS 183

Db 2122 GRCDPHTGRCNC-----PPGLSGERCDCSCQHQVVPVPGGPVGH 2161

Qy 184 L 184

Db 2162 I 2162

RESULT 27

VT2\_SFVKA

ID VT2\_SFVKA STANDARD; PRT; 325 AA.

AC P25943;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tumor necrosis factor soluble receptor precursor (Protein T2).

GN T2.

OS Shope fibroma virus (strain Kasza) (SFV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Leporipoxvirus.

OX NCBI\_TaxID=10272;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=87321103; PubMed=2820128;

RA Upton C., Delange A.M., McFadden G.;

RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome.";

RL Virology 160:20-30(1987).

RN [2]

RP FUNCTION.

RX MEDLINE=91207415; PubMed=1850261;

RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,

RA McFadden G., Goodwin R.G.;

RT "T2 open reading frame from the Shope fibroma virus encodes a soluble form of the TNF receptor.";

RL Biochem. Biophys. Res. Commun. 176:335-342(1991).

CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -----

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CC -----

DR EMBL; M17433; -; NOT ANNOTATED\_CDS.

DR EMBL; A23727; CA01657.1; -.

DR PIR; B43692; B43692.

DR HSSP; P19438; 1EXT.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 2.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.

KW Receptor; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.

FT REPEAT 27 62 TNFR-CYS 1.

FT REPEAT 63 104 TNFR-CYS 2.

FT REPEAT 105 147 TNFR-CYS 3.

FT REPEAT 148 186 TNFR-CYS 4.

FT DISULFID 28 39 BY SIMILARITY.

FT DISULFID 40 53 BY SIMILARITY.

FT DISULFID 43 61 BY SIMILARITY.

FT DISULFID 64 79 BY SIMILARITY.

FT DISULFID 82 96 BY SIMILARITY.

FT DISULFID 86 104 BY SIMILARITY.

FT DISULFID 106 120 BY SIMILARITY.

FT DISULFID 123 146 BY SIMILARITY.

FT DISULFID 129 149 BY SIMILARITY.

FT DISULFID 164 185 BY SIMILARITY.

FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 205 205 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 9.8%; Score 140.5; DB 1; Length 325;

Best Local Similarity 27.6%; Pred. No. 0.00015;

Matches 43; Conservative 12; Mismatches 54; Indels 47; Gaps 8;

Qy 28 CDNCQPGTFCRKY-----NPVCKSCPSTF-SSIGGQPNICR-VCAGYFRKKFCSST 80

Db 40 CASCHFGFYASRLCGPSNTVCSPECDGTFTASTNHAPACVSCRGPCCTGHLSESQPCDRT 99

Qy 81 HNAECECEIEGFHCLGPQCTRCCKDCRPGQELTKQCKTCSLGTFTNDQNGTGVCRPWTNC- 139

Db 100 HDRVCNCSTGNYCL-----LKGQNGCRICAPQTKCP 130

Qy 140 ---SLDGRSVLKTGT--EKDVVCGPPVVSFSPSTT 170

Db 131 AGYGVSGHT--RAGDTLCEK---CPPHTYSDLSPT 161

RESULT 28

TR16\_CHICK

ID TR16\_CHICK STANDARD; PRT; 416 AA.

AC P18519;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR) (p75 ICD) (Low affinity neurotrophin receptor p75NTR).

DE NGFR OR TNFRSF16.

GN Gallus gallus (Chicken).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=90166579; PubMed=2560385;

RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,

RA Shooter E.M., Reichardt L.F.;

RT "Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system.";

RT Neuron 2:1123-1134(1989).

RN [2]

RP SEQUENCE OF 21-416 FROM N.A.

RX MEDLINE=90152140; PubMed=2154393;

RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;

RT "Structure and developmental expression of the chicken NGF receptor.";

RL Dev. Biol. 137:287-304(1990).

CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3, and NT-4. Can mediate cell survival as well as cell death of neural cells (By similarity).

CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-associated cell death executor. Interacts with TRAF2, TRAF4, TRAF6 and PTPN13 (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- PTM: N- and O-glycosylated.

CC -!- PTM: Phosphorylated on serine residues.

```
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -1- SIMILARITY: Contains 1 death domain.
DR PIR; JN0006; JN0006.
DR HSSP; P07174; INGR.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW Repeat; Phosphorylation; Signal.
FT SIGNAL 1 19
FT CHAIN 20 416
FT
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 16.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 29 239
FT DOMAIN 240 261
FT TRANSMEM 262 416
FT REPEAT 23 57
FT REPEAT 58 99
FT REPEAT 100 138
FT REPEAT 140 180
FT REPEAT 333 410
FT DOMAIN 188 236
FT DOMAIN 24 35
FT DISULFID 36 49
FT DISULFID 39 56
FT DISULFID 59 75
FT DISULFID 78 91
FT DISULFID 81 99
FT DISULFID 101 114
FT DISULFID 117 130
FT DISULFID 120 138
FT DISULFID 141 156
FT DISULFID 159 172
FT DISULFID 162 180
FT CARBOHYD 52 52
FT CONFLICT 36 36
FT CONFLICT 173 173
FT CONFLICT 276 276
FT CONFLICT 396 396
SQ SEQUENCE 416 AA; 44654 MW; 6BCEAABS4P4D2D56 CRC64;

Query Match 9.8%; Score 139.5; DB 1; Length 416;
Best Local Similarity 25.7%; Pred. No. 0.00022;
Matches 53; Conservative 24; Mismatches 82; Indels 47; Gaps 12;

QY 9 VVIVLLLVGCEKVGAVQNSDNC-----QPQTFCKYN-----PVCKSCPP 49
Db 5 VPLLLLLL---PAGPTWGSKEKCLTKMYTTSGECCACNLGEGVQPCGVNQTVCEPCLD 61
QY 50 S-TFS-SIGGQNCNICRVCAGYFRFKKFCSTHNAECEIEGF-----HCLGPQCTR 100
Db 62 SVTYSDTVSAATEPCCKPCTQCQVGLHSMSPCVESDDAVCRCAYGTFQDELSGSC--KECSI 119
QY 101 CEK-----DCRPGQELTKQCKTCSLGTENDQ-NGTGVCRPWTNCSLDGRSVLKTGTTE 153
Db 120 CEVGFGLMFPCKDSQDTV---CEECPEGTFSDEANFVDPCLPTICE-ENEVMVKECTAT 175
QY 154 KDVVV---GPPVVSFSPSTTISVTPE 176
Db 176 SDAECRDHLHPRWTHTPSLAGSDSPE 201

RESULT 29
CRMB_VARV STANDARD; PRT; 349 AA.
ID CRMB_VARV
AC P34015; Q85407; Q89098; Q89118;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
```

```
DT -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
DE Soluble TNF receptor II precursor (cytokine response modifying protein
DE B).
GN CRMB OR G2R OR G4R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N.; Blinov V.M.; Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bangladesh-1975;
RX MEDLINE=94088747; PubMed=8264798;
RA Massung R.F.; Esposito J.J.; Liu L.; Qi J.; Utterback T.R.;
RA Knight J.C.; Aubin L.; Yuran T.E.; Parsons J.M.; Loparev V.N.;
RA Selivanov N.A.; Cavallaro K.F.; Kerlavage A.R.; Mahy B.W.J.;
RA Venter C.J.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome.";
RL Nature 366:748-751(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Garcia-1966, and Somalia-1977;
RA Massung R.F.; Loparev V.N.; Knight J.C.; Chizhikov V.E.; Parsons J.M.;
RA Totmenin A.V.; Shchelkunov S.N.; Esposito J.J.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Garcia-1966;
RX MEDLINE=20107289; PubMed=10639322;
RA Shchelkunov S.N.; Totmenin A.V.; Loparev V.N.; Safronov P.F.;
RA Gutorov V.V.; Chizhikov V.E.; Knight J.C.; Parsons J.M.; Massung R.F.;
RA Esposito J.J.;
RT "Alastrim smallpox variola minor virus genome DNA sequences.";
RL Virology 266:361-386(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
RA Loparev V.N.; Parsons J.M.; Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC the modification of TNF-mediated antiviral processes (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC
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CC
CC EMBL; X69198; CAA49137.1; -
DR EMBL; X67117; CAA47540.1; -
DR EMBL; L22579; AAA60933.1; -
DR EMBL; U18339; AAA69407.1; -
DR EMBL; U18341; AAA69467.1; -
DR EMBL; Y16780; CAB54798.1; -
DR EMBL; U88146; AAB94371.1; -
DR EMBL; U88148; AAB94373.1; -
DR EMBL; U88149; AAB94374.1; -
DR EMBL; U88152; AAB94377.1; -
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DR PIR; D36858; D36858.
DR PIR; D72175; D72175.
DR PIR; T28623; T28623.
DR HSP; O14763; 1D0G.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 349 SOLUBLE TNF RECEPTOR II.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
FT DISULFID 32 43 BY SIMILARITY.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 65 BY SIMILARITY.
FT DISULFID 68 83 BY SIMILARITY.
FT DISULFID 86 100 BY SIMILARITY.
FT DISULFID 90 108 BY SIMILARITY.
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 17 17 MISSING (IN STRAINS BANGLADESH-1975 AND
FT VARIANT 160 160 H -> Y (IN STRAINS BUTLER-1952, GARCIA-
FT VARIANT 165 165 1966 AND SOMALIA-1977).
FT VARIANT 182 182 A -> T (IN STRAINS BUTLER-1952 AND
FT VARIANT 274 274 GARCIA-1966).
FT VARIANT 335 335 E -> K (IN STRAIN SOMALIA-1977).
FT VARIANT 339 339 A -> E (IN STRAIN SOMALIA-1977).
FT VARIANT 339 339 N -> D (IN STRAINS BUTLER-1952 AND
FT VARIANT 339 339 GARCIA-1966).
FT VARIANT 339 339 P -> L (IN STRAINS BUTLER-1952 AND
FT SEQUENCE 349 AA; 38189 MW; D45D40B5C6E780EF CRC64;

Query Match 9.7%; Score 138; DB 1; Length 349;
Best Local Similarity 22.6%; Pred. No. 0.00025;
Matches 59; Conservative 28; Mismatches 104; Indels 70; Gaps 11;

QY 28 CDNCPGTFC-----RKYNPVCKSPPTFSSIGGQ-PNCNICR-VCAGYFRFKFCSST 80
Dd 44 CLSCPGTYASRLCDSKTNTQCTCGSGTFTSRNNHLPACLSGRCNSNQVETRSCNTT 103
QY 81 HNAECIEGFHCL---GPQCTRCCKDCRPGQELTKQG-----CKTCSLGTFDNQ-N 128
Dd 104 HNRICECPGYCLLKSGGCKACVSQTKGIGYGVSGHTSVGDVICSPPCGGTYSHTVS 163
QY 129 GTGVCRPWTNCLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGGPGHSLQVLT 188
Dd 164 SADKCEPVPNNTFNVIDVEITLYPVNDTSC-----TRTTTGLSES----- 204
QY 189 LFLALTSALLAL-----IFITLLFSLVKWI-----RKFPFHFK----- 223
Dd 205 ---ILTSELITNMHTDCNPVREBYFSLNKKVATSGFTGENTRYQNIISKVCTLNFEIKC 261
QY 224 ----QPFKTTGAQAEEDACS 240
Dd 262 NNKGSSFKQLTKARNDDGMS 282

RESULT 30
LMA2_MOUSE
ID LMA2_MOUSE STANDARD; PRT; 3106 AA.
AC Q60675; Q05003; Q64061;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy
chain).
```

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GN LAMA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Embryo, and Heart;
RX MEDLINE=95316259; PubMed=7795883;
RA Bernier S.M., Utani A., Sugiyama S., Doi T., Polistina C.,
RA Yamada Y.;
RT "Cloning and expression of laminin alpha 2 chain (M-chain) in the
RT mouse.";
RL Matrix Biol. 14:447-455(1995).
RN [2]
RP SEQUENCE OF 2162-2279 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Thymus;
RX MEDLINE=93346725; PubMed=8345183;
RA Chang A.C., Wadsworth S., Coligan J.E.;
RT "Expression of merosin in the thymus and its interaction with
RT thymocytes.";
RL J. Immunol. 151:1789-1801(1993).
RN [3]
RP SEQUENCE OF 54-281 FROM N.A.
RX MEDLINE=95179178; PubMed=7874173;
RA Xu H., Wu X.R., Wewer U.M., Engvall E.;
RT "Murine muscular dystrophy caused by a mutation in the laminin alpha
RT 2 (Lama2) gene.";
RL Nat. Genet. 8:297-302(1994).
RN [4]
RP SEQUENCE OF 20-25.
RX MEDLINE=21818471; PubMed=11829758;
RA Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.;
RT "Complete sequence, recombinant analysis and binding to laminins and
RT sulphated ligands of the N-terminal domains of laminin alpha3B and
RT alpha5 chains.";
RL Biochem. J. 362:213-221(2002).
RN [5]
RP BINDING TO FBLN1, FBLN2, AND NID2.
RX MEDLINE=99146904; PubMed=10022829;
RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
RT "Binding of the G domains of laminin alpha1 and alpha2 chains and
RT perlecan to heparin, sulfatides, alpha-dystroglycan and several
RT extracellular matrix proteins.";
RL EMBO J. 18:863-870(1999).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 2932-3106.
RX MEDLINE=20085745; PubMed=10619025;
RA Hohenester E., Tisi D., Talts J.F., Timpl R.;
RT "The crystal structure of a laminin G-like module reveals the
RT molecular basis of alpha-dystroglycan binding to laminins, perlecan,
RT and agrin.";
RL Mol. Cell 4:783-792(1999).
CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The alpha-2 chain is a subunit of laminin-2 (Merosin) and
CC laminin-4 (S-merosin). Interacts with FBLN1, FBLN2 and NID2.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes (major
CC component).
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI, IV and G are globular.
CC -!- DISEASE: Defects in LAMA2 are a cause of murine muscular dystrophy
CC (dy2J).
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 17 laminin EGF-like domains.
```



DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Major surface-labeled trophozoite antigen 417 precursor.  
GN TSA 417.  
OS Giardia lamblia (Giardia intestinalis).  
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.  
OX NCBI\_TaxID=5741;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 30957 / WB;  
RX MEDLINE=90280395; PubMed=2352929;  
RA Gillin F.D., Hagblom P., Harwood J., Aley S.B., Reiner D.S.,  
RA McCaffery M., So M., Guiney D.G.;  
RT "Isolation and expression of the gene for a major surface protein of  
RT Giardia lamblia";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:4463-4467(1990).  
RN [2]  
RP SEQUENCE OF 480-620 FROM N.A.  
RC STRAIN=AD-1;  
RX MEDLINE=93314970; PubMed=8325510;  
RA Ey P.L., Mayrhofer G.;  
RT "Two genes encoding homologous 70-kDa surface proteins are present  
RT within individual trophozoites of the binucleate protozoan parasite  
RT Giardia intestinalis";  
RL Gene 129:257-262(1993).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane.  
CC -!- DOMAIN: CONTAINS 29 REPEATS OF THE CXXC MOTIF.  
CC -!- SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.  
CC  
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CC -----  
DR EMBL; M33641; AAA02688.1; -  
DR EMBL; M97488; AAA02581.1; -  
DR PIR; A35502; A35502.  
DR PIR; PC1294; PC1294.  
DR InterPro; IPR006212; Furin\_repeat.  
DR InterPro; IPR005127; Giardia\_VSP.  
DR InterPro; IPR009030; Grow\_fac\_recep.  
DR InterPro; IPR006210; IEGF.  
DR Pfam; PF03302; VSP; 1.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00261; FU; 3.  
DR Signal; Antigen; Glycoprotein; Transmembrane; Repeat.  
FT SIGNAL 1 17  
FT CHAIN 18 713 MAJOR SURFACE-LABELED TROPHOZOITE  
FT ANTIGEN 417.  
FT DOMAIN 18 679 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 680 708 POTENTIAL.  
FT DOMAIN 709 713 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 676 676 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 582 582 A -> T (IN STRAIN ADELAIDE-1).  
FT VARIANT 606 606 A -> S (IN STRAIN ADELAIDE-1).  
SQ SEQUENCE 713 AA; 72510 MW; 9AD7195843DE5601 CRC64;  
  
Query Match 9.5%; Score 135.5; DB 1; Length 713;  
Best Local Similarity 25.6%; Pred. No. 0.00081;  
Matches 58; Conservative 20; Mismatches 67; Indels 82; Gaps 15;  
  
QY 15 LVGCE-----KVGAVQNSCD---NCQ-PGTFGR-----KYNPVKSCPPSTPSSIGGQ 58  
Db 312 LVTCSACTDGYKPSADKTCCEAVSNCKTPG--CKACNKGKNEVCTDCDGSYLTPTSQ 369  
QY 59 PNC-NICRVCAGYF---RPFKFCSSTHNAECE-----CIEGFHCLGPQCTRCEK 103  
Db 370 --CIDSCAKIGNYYGATEAKKLCKECTAANCKTCDQGCQACNDGFYKNGDACSPCH- 426

QY 104 DCRPGQLTKQGCKTKCSLGTEND-----QNGTGYCRPW 136  
Db 427 -----ESCKTCSAGTASDCTECPTGKALRYGDDGTGKTCGEGCTTGTGAGACK-- 474  
QY 137 TNCSL--DGRSVLK--TGTTE--KDVVCGPPVVSFSPSTTISVTPEG 177  
Db 475 -TCGLTIDGASYCSECATTTTEYPQNGVCAPKASRATPTCNDSPIQNG 520  
  
RESULT 32  
LMA2\_HUMAN  
ID LMA2\_HUMAN STANDARD; PRT; 3110 AA.  
AC P24043; Q14736; Q93022;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Laminin alpha-2 chain precursor (laminin M chain) (Merosin heavy  
DE chain).  
GN LAMA2 OR LAMM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=94124633; PubMed=8294519;  
RA Vuolteenaho R., Nissinen M., Sainio K., Byers M., Eddy R.,  
RA Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K.;  
RT "Human laminin M chain (merosin): complete primary structure,  
RT chromosomal assignment, and expression of the M and A chain in human  
RT fetal tissues.";  
RL J. Cell Biol. 124:381-394(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97066955; PubMed=8910357;  
RA Zhang X., Vuolteenaho R., Tryggvason K.;  
RT "Structure of the human laminin alpha2-chain gene (LAMA2), which is  
RT affected in congenital muscular dystrophy.";  
RL J. Biol. Chem. 271:27664-27669(1996).  
RN [3]  
RP SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=90238994; PubMed=2185464;  
RA Ehrig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E.;  
RT "Merosin, a tissue-specific basement membrane protein, is a  
RT laminin-like protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).  
RN [4]  
RP VARIANTS GIN-545; HIS-619; LEU-919; HIS-2586 AND LYS-2614.  
RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,  
RA Marzluf G.A., Amato A.A., Mendell J.R.;  
RT "Novel single base polymorphisms and rare sequence variants in  
RT the laminin 2-chain coding region detected by RNA/SSCP analysis.";  
RL Hum. Mutat. 13:174-174(1999).  
RN [5]  
RP ERRATUM.  
RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,  
RA Marzluf G.A., Amato A.A., Mendell J.R.;  
RL Hum. Mutat. 13:340-340(1999).  
RN [6]  
RP VARIANT MDC1A PRO-2564.  
RX MEDLINE=21476011; PubMed=11591858;  
RA He Y., Jones K.J., Vignier N., Morgan G., Chevally M., Barois A.,  
RA Estournet-Mathiaud B., Hori H., Mizuta T., Tome F.M.S., North K.N.,  
RA Guicheney P.;  
RT "Congenital muscular dystrophy with primary partial laminin alpha-2  
RT chain deficiency: molecular study.";  
RL Neurology 57:1319-1322(2001).  
RN [7]  
RP VARIANTS MDC1A TYR-527 AND ARG-862.  
RX MEDLINE=22439669; PubMed=12552556;





FT DISULFID 86 99 BY SIMILARITY.  
FT DISULFID 89 107 BY SIMILARITY.  
FT DISULFID 109 122 BY SIMILARITY.  
FT DISULFID 125 138 BY SIMILARITY.  
FT DISULFID 128 146 BY SIMILARITY.  
FT DISULFID 149 164 BY SIMILARITY.  
FT DISULFID 167 180 BY SIMILARITY.  
FT DISULFID 170 188 BY SIMILARITY.  
FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 427 AA; 45183 MW; B09PA143FB3D625B CRC64;  
  
Query Match 9.5%; Score 135; DB 1; Length 427;  
Best Local Similarity 25.2%; Pred. No. 0.00054;  
Matches 65; Conservative 26; Mismatches 97; Indels 70; Gaps 15;  
  
QY 10 VIVLLVGEKVGAVQ-----NSCDNCPQGT-----CRKYNPVCKSCPPS-TFS 53  
Db 15 LLLLLLLVSLGGAKEACPTGLYTHSGECKACKNLGEGVAQPCGANQTVCEPCLDSVTF 74  
QY 54 S-IGGPNPCNICRVAGYFRFKKCSSTHNAECEIEGFHCLGPGQCTRC--KDCRPGQE 110  
Db 75 DVVSATEPKPCTECVGLQMSAPCVDADAVCRCAAGY-QDETTGRCEACRVCEAGSG 133  
QY 111 LT-----KQG--CKTSLGTFTNDQ-NGTGVCRPWTNCSLDGRSVLKTGTEKDVVC----- 158  
Db 134 LVFSCQDKQNTVCBPCPDGTYSDEANHVDPCLPCTVCE-DTERQLRECTRWADAECEIEP 192  
QY 159 -----GPPVVSFS--PSTTISVTPEGGPG-----GHSLOVLT----- 188  
Db 193 GRWITRSTPEGSDSTAPSTQ---EPEAPPEQDLIASTVAGVVVTVMGSSQPVVTRGTGD 249  
QY 189 ----LFLALTSALLALI 202  
Db 250 NLIPVYCSILAAVVVGLV 267

RESULT 34  
ITB5\_PAPCY STANDARD; PRT; 655 AA.  
AC Q07441;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Integrin beta-5 (Fragment).  
GN ITGB5.  
OS Papio cynocephalus (Yellow baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheciae; Papio.  
OX NCBI\_TaxID=9556;  
RN [1]\_TaxID=9556;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94040831; PubMed=8224922;  
RA Shoji M., Hayzer D.J., Kim T.M., Runge M.S., Hanson S.R.;  
RT "Human and baboon integrin beta 5 subunit-encoding mRNAs have  
alternative polyadenylation sites.";  
RL Gene 133:307-308(1993).  
CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.  
CC IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.  
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5  
CC ASSOCIATES WITH ALPHA-V.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- PTM: The cysteine residues are involved in intrachain disulfide  
CC bonds.  
CC -!- SIMILARITY: Belongs to the integrin beta chain family.  
CC -!- SIMILARITY: Contains 2 WFA-like domains.  
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CC -----  
DR EMBL; L12231; AAA16866.1; -.  
DR HSSP; P05106; LJV2.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR002369; Integrin B.  
DR InterPro; IPR001169; Integrin\_beta\_C.  
DR InterPro; IPR002035; VWF A.  
DR Pfam; PF00362; integrin\_B; 1.  
DR PRINTS; PR01186; INTEGRIN.  
DR ProDom; PD001811; Integrin\_B; 1.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00187; INB; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS00243; INTEGRIN\_BETA; 2.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_2.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;  
KW Repeat; Extracellular matrix; Cytoskeleton.  
FT NON\_TER 1  
FT DOMAIN <1 575 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 576 598 POTENTIAL.  
FT DOMAIN 599 655 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN <1 234 WFA-LIKE.  
FT DOMAIN 457 621 4 CYSTEINE-RICH TANDEM REPEATS.  
FT REPEAT 321 368 I.  
FT REPEAT 369 410 II.  
FT REPEAT 411 449 III.  
FT REPEAT 450 486 IV.  
FT CARBOHYD 203 203 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 316 316 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 408 408 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 442 442 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 510 510 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 561 561 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 655 AA; 72466 MW; BAC33A159CBE1596 CRC64;  
  
Query Match 9.5%; Score 135; DB 1; Length 655;  
Best Local Similarity 27.7%; Pred. No. 0.00082;  
Matches 64; Conservative 30; Mismatches 93; Indels 44; Gaps 14;  
  
QY 27 SCDNCQ--PCTFCRKYNPVCK---SCP--PSTFSSIGGQPNICRVAGYFRFKKPCS 78  
Db 385 SCNQCSESEFGKIYGFCECDNFSCARNKGVLCGSGHGECHGAGYIGDNCNC- 443  
QY 79 STHNAECE-----CIEGFHCLGPGQ-----TFCEK--DCRPGQELTKQGCKTCSL 121  
Db 444 STDISTCRGRDGOICSEGRHCLGQCGQCTEPGAFGECKEKCPTC-PDACSTKRDCECPL 502  
QY 122 ---GTFNDQNGTGVCVCR---PWTNCSL--DGRSVLKTGTTTEKDVVCGPPVW---SFSPT 169  
Db 503 LHSKPDNQCHSLCRDEVITWVDTIVKDDQEAVALCYFKTAKDCVMFTYVELPSGKSNL 562  
QY 170 TISVTPGEGPGHSLQVLTFLALTSALLLALIFITLLFSLVKWI--RKKF 218  
Db 563 TVLREPE---CGNTPNAMILLAVGSIILVGLALLAIWKLIVTIDHREF 610

RESULT 35  
T10D\_HUMAN STANDARD; PRT; 386 AA.  
AC Q9UBN6; Q9Y6Q4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10D precursor (Decoy  
DE receptor 2) (DcR2) (TNF-related apoptosis-inducing ligand receptor 4)  
DE (TRAIL receptor-4) (TRAIL-R4) (TRAIL receptor with a truncated death  
DE domain).  
GN TNFRSF10D OR DCR2 OR TRAILR4 OR TRUND4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND VARIANT.  
RC TISSUE=Fetal lung;  
RX MEDLINE=98044290; PubMed=9382840;

RA Marsters S.A., Sheridan J.P., Pitti R.M., Huang A., Skubatch M.,  
RA Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P.,  
RA Ashkenazi A.;

RT "A novel receptor for Apo2L/TRAIL contains a truncated death domain."  
RL Curr. Biol. 7:1003-1006(1997).

RN [2]

RP SEQUENCE FROM N.A., CHARACTERIZATION, AND VARIANTS SER-35 AND LEU-310.  
RC TISSUE=Foreskin fibroblast, and peripheral blood lymphocytes;  
RX MEDLINE=98090091; PubMed=9430226;

RA Degli-Esposti M.A., Dougall W.C., Smolak P.J., Waugh J.Y., Smith C.A.,  
RA Goodwin R.G.;

RT "The novel receptor TRAIL-R4 induces NF-kappaB and protects against  
RT TRAIL-mediated apoptosis, yet retains an incomplete death domain."  
RL Immunity 7:813-820(1997).

RN [3]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC MEDLINE=98196860; PubMed=9537512;

RA Pan G., Ni J., Yu G.-L., Wei Y.-F., Dixit V.M.;

RT "TRUND, a new member of the TRAIL receptor family that antagonizes  
RT TRAIL signalling."

RL FEBS Lett. 424:41-45(1998).

RN [4]

RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=2238257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Contains a  
CC truncated death domain and hence is not capable of inducing  
CC apoptosis but protects against TRAIL-mediated apoptosis. Reports  
CC are contradictory with regards to its ability to induce the NF-  
CC kappaB pathway (According to Ref.1 it cannot but according to  
CC Ref.2 it can induce the NF-kappa-B pathway).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Widely expressed, in particular in fetal  
CC kidney, lung and liver, and in adult testis and liver. Also  
CC expressed in peripheral blood leukocytes, colon and small  
CC intestine, ovary, prostate, thymus, spleen, pancreas, kidney,  
CC lung, placenta and heart.

CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.

CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; AF029761; AAD03477.1; -  
DR EMBL; AF021232; AAC32765.1; -  
DR EMBL; AF021233; AAC32766.1; -  
DR EMBL; AF023849; AAC52053.1; -  
DR EMBL; BC052270; AAH52270.1; -  
DR HSSP; O14763; 1D4V.  
DR Genew; HGNC:11907; TNFRSF10D.  
DR MIM; 603614; -  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_2; 2.  
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;  
KW Polymorphism.  
FT SIGNAL 1 55  
FT CHAIN 56 386  
FT DOMAIN 56 211  
FT TRANSMEM 212 232  
FT DOMAIN 233 386  
FT REPEAT 58 97  
FT REPEAT 98 139  
FT REPEAT 140 180  
FT DOMAIN 340 366  
FT DOMAIN 225 228  
FT DOMAIN 246 250  
FT DISULFID 83 96  
FT DISULFID 99 115  
FT DISULFID 118 131  
FT DISULFID 121 139  
FT DISULFID 141 155  
FT DISULFID 158 172  
FT DISULFID 162 180  
FT CARBOHYD 127 127  
FT CARBOHYD 182 182  
FT VARIANT 35 35  
FT VARIANT 310 310  
FT SEQUENCE 386 AA; 41823 MW; 77A93577CAAF2632 CRC64;  
SQ  
Query Match 9.4%; Score 134.5; DB 1; Length 386;  
Best Local Similarity 22.7%; Pred. No. 0.00054;  
Matches 54; Conservative 29; Mismatches 78; Indels 77; Gaps 11;  
QY 29 DNCQPGTFCRKYNPVCKSPSTFSSIGGQ--PNCNICRVCAGYFRKKFKCSSTHNAECE 86  
Db 81 EECFAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQ 140  
QY 87 CIEGFHCLGPQCTRCCKDCRPGQELTKQCKTCSLGFNDQNGTGVCRPW-TNCSLDGRS 145  
Db 141 -----CEK-----GSFQDKNSPEMCRCTCTGCP---RG 165  
QY 146 VLKGTG--TTEKDVVCGPPVWSFSPSTTISVTPEGGPGHSLQVLTFLALTSALLALIF 203  
Db 166 MVKVSNCPTSRDIKC-----KNESAASSTGKTPA-----AETVTILGMLASPHYLLI 215  
QY 204 ITLLFSVLKWI-----RKKFPHIFKQPFKKTGAQEEADACSCRCPEEGGGGGE 255  
Db 216 IVLVITILAVVVVGVGFSCKRKKFISYLK-----GICS-----GGGGGPE 252  
RESULT 36  
ITB5\_HUMAN  
ID ITB5\_HUMAN STANDARD; PRT; 799 AA.  
AC P18084;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Integrin beta-5 precursor.  
GN ITGB5.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thymic epithelium;  
RX MEDLINE=90228356; PubMed=2328726;  
RA Ramaswamy H., Kemler M.E.;  
RT "Cloning, primary structure and properties of a novel human integrin  
beta subunit.";  
RL EMBO J. 9:1561-1568(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90319111; PubMed=2371275;  
RA Suzuki S., Huang Z.S., Tanihara H.;  
RT "Cloning of an integrin beta subunit exhibiting high homology with  
integrin beta 3 subunit.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5354-5358(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91009141; PubMed=2211615;  
RA McLean J.W., Vestal D.J., Cheres D.A., Bodary S.C.;  
RT "cDNA sequence of the human integrin beta 5 subunit.";  
RL J. Biol. Chem. 265:17126-17131(1990).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.  
CC IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.  
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5  
CC ASSOCIATES WITH ALPHA-V.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the integrin beta chain family.  
CC -!- SIMILARITY: Contains 2 VWFA-like domains.  
CC -----  
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CC -----  
CC EMBL; X53002; CAA37188.1; -  
CC EMBL; M35011; AAA52707.1; -  
CC EMBL; J05633; AAA59183.1; -  
CC EMBL; BC006541; AAH06541.1; -  
CC PIR; A38308; A38308.  
CC HSP; P05106; 1JUV2.  
CC Genew; HGNC:6160; ITGB5.  
CC MIM; 147561; -

DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR002369; Integrin\_B.  
DR InterPro; IPR001169; Integrin\_beta\_C.  
DR InterPro; IPR003659; Plexin-like.  
DR InterPro; IPR002035; VWF A.  
DR Pfam; PF00362; integrin\_B; 1.  
DR PRINTS; PR01186; INTEGRINB.  
DR ProDom; PD001811; Integrin\_B; 1.  
DR SMART; SM00187; INB; 1.  
DR SMART; SM00423; PSI; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS00243; INTEGRIN\_BETA; 2.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_2.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_2.  
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;  
KW Repeat; Signal.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 799 INTEGRIN BETA-5.  
FT DOMAIN 24 719 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 720 742 POTENTIAL.  
FT DOMAIN 743 799 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 136 378 VWFA-LIKE.  
FT DOMAIN 465 630 4 CYSTEINE-RICH TANDEM REPEATS.  
FT REPEAT 465 512 I.  
FT REPEAT 513 554 II.  
FT REPEAT 555 593 III.  
FT REPEAT 594 630 IV.  
FT DISULFID 28 463 BY SIMILARITY.  
FT DISULFID 36 46 BY SIMILARITY.  
FT DISULFID 39 75 BY SIMILARITY.  
FT DISULFID 49 64 BY SIMILARITY.  
FT DISULFID 202 211 BY SIMILARITY.  
FT DISULFID 259 300 BY SIMILARITY.  
FT DISULFID 401 413 BY SIMILARITY.  
FT DISULFID 433 682 BY SIMILARITY.  
FT DISULFID 461 465 BY SIMILARITY.  
FT DISULFID 476 487 BY SIMILARITY.  
FT DISULFID 484 522 BY SIMILARITY.  
FT DISULFID 489 498 BY SIMILARITY.  
FT DISULFID 500 513 BY SIMILARITY.  
FT DISULFID 528 533 BY SIMILARITY.  
FT DISULFID 530 563 BY SIMILARITY.  
FT DISULFID 535 548 BY SIMILARITY.  
FT DISULFID 550 555 BY SIMILARITY.  
FT DISULFID 569 574 BY SIMILARITY.  
FT DISULFID 571 602 BY SIMILARITY.  
FT DISULFID 576 585 BY SIMILARITY.  
FT DISULFID 587 594 BY SIMILARITY.  
FT DISULFID 608 613 BY SIMILARITY.  
FT DISULFID 610 657 BY SIMILARITY.  
FT DISULFID 615 625 BY SIMILARITY.  
FT DISULFID 628 631 BY SIMILARITY.  
FT DISULFID 635 644 BY SIMILARITY.  
FT DISULFID 641 714 BY SIMILARITY.  
FT DISULFID 661 690 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 460 460 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 505 505 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 552 552 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 586 586 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 654 654 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 705 705 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 193 193 T -> A (IN REF. 2).  
FT CONFLICT 645 645 L -> P (IN REF. 3).  
FT CONFLICT 790 792 MISSING (IN REF. 2).  
FT SEQUENCE 799 AA; 88053 MW; D7E4727CA310512B CRC64;  
SQ

Query Match 9.4%; Score 134; DB 1; Length 799;  
Best Local Similarity 27.7%; Pred. No. 0.0012;  
Matches 64; Conservative 30; Mismatches 93; Indels 44; Gaps 14;

OY 27 SCDNCQ--PGTFCRKNVPCK-----SCP--PSTFSSIGGQPNICRVCAGYFRFKKPCS 78

Db 529 SCNQSCFESEFGKIYGFCECDNFSCARNKGVLCSGHGECHGCKCHAGYIGDNCNC- 587  
 Qy 79 STHNAECE-----CIEGFHCLGPOC-----TRCEK--DCRPGQELTKQCKTKCSL 121  
 Db 588 STDISTCRGRDQICSGRCHCLGQCCQCTEPGAFGEMCEKPTC-PDACSTKRDCEVCLL 646  
 Qy 122 ---GTFNDQNGTGVCR---PWTNCSL--DGRSVLKTGTTEKDVVCGPPVW---SFSPT 169  
 Db 647 LHSGKPDNQCHSLCRDEVITWDTIVKDDQEAVALCFYKTAKDCVMFTYVELPSPGKSNL 706  
 Qy 170 TISVTEGGPGGSHSLQVLTFLALTSALLLALIFITLLFSVLKWI--RKKF 218  
 Db 707 TVLREPE---CGTNPAMTILLAVVGSILLVGLALLAIWKLLVTHIDRREF 754

RESULT 37  
 CRMB\_COWPX STANDARD; PRT; 351 AA.  
 AC 073559; P87602;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Soluble TNF receptor II precursor (cytokine response modifying protein B).  
 GN (CRMB1 OR D2L) AND (CRMB2 OR I4R).  
 OS Cowpox virus (CPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=10243;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GRI-90 / Grishak;  
 RX MEDLINE=98229462; PubMed=9568042;  
 RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,  
 RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;  
 RT "The genomic sequence analysis of the left and right species-specific  
 RT terminal region of a cowpox virus strain reveals unique sequences and  
 RT a cluster of intact ORFs for immunomodulatory and host range  
 RT proteins.";  
 RL Virology 243:432-460(1998).  
 RN [2]  
 RP FUNCTION.  
 RC STRAIN=Brighton red;  
 RX MEDLINE=94378510; PubMed=8091665;  
 RA Hu F.Q., Smith C.A., Pickup D.J.;  
 RT "Cowpox virus contains two copies of an early gene encoding a soluble  
 RT secreted form of the type II TNF receptor.";  
 RL Virology 204:343-356(1994).  
 CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to  
 CC the modification of TNF-mediated antiviral processes.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.  
 CC  
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 CC  
 CC EMBL; X94355; CAA64087.2; -  
 CC EMBL; X94355; CAD90756.1; -  
 CC HSSP; O14763; 1D0G.  
 CC InterPro; IPR001368; TNFR\_c6.  
 CC Pfam; PF00020; TNFR\_c6; 2.  
 CC SMART; SM00208; TNFR; 3.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 CC PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 CC Receptor; Glycoprotein; Repeat; Signal.  
 CC SIGNAL 1 19 POTENTIAL.  
 CC CHAIN 20 351 SOLUBLE TNF RECEPTOR II.

FT REPEAT 31 67 TNFR-CYS 1.  
 FT REPEAT 69 110 TNFR-CYS 2.  
 FT DISULFID 32 43 BY SIMILARITY.  
 FT DISULFID 44 57 BY SIMILARITY.  
 FT DISULFID 47 67 BY SIMILARITY.  
 FT DISULFID 70 85 BY SIMILARITY.  
 FT DISULFID 88 102 BY SIMILARITY.  
 FT DISULFID 92 110 BY SIMILARITY.  
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 351 AA; 38253 MW; 57CAE73EF4ESD7C7 CRC64;  
 Query Match 9.3%; Score 133.5; DB 1; Length 351;  
 Best Local Similarity 29.5%; Pred. No. 0.00059;  
 Matches 38; Conservative 14; Mismatches 56; Indels 21; Gaps 8;  
 QY 28 CDNCOPGTFCRKY-----NPVCKSCPPSTFSSIGGQ-PNCNCR-VCAGYFRFKFCS 78  
 Db 44 CLSCPPGTIYASRLCDSKTNTNTQTCTPCGSGTFTSRNNHLPACLSGRCDSNQVETRSCN 103  
 QY 79 STHNAECEIEGFHCL--GPOCTRC--EKDPRPGQEL---TKQG---CKTCSLGTENDQ 127  
 Db 104 TTHNRICECAPGYVLLKGGSSGCKACVSQTKCGIGYGVSGHTSTGVDVCSGCLGTYSHT 163  
 QY 128 -NGTGVCRP 135  
 Db 164 VSSADKCEP 172  
 RESULT 38  
 TNFR6\_PIG STANDARD; PRT; 332 AA.  
 AC O77736;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL  
 DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)  
 DE (CD95).  
 GN TNFRSF6 OR APT1 OR FAS.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
 RT "Expression of apoptosis-associated genes in hibernating and stunned  
 RT myocardium of pig.";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD  
 CC recruits caspase-8 to the activated receptor. The resulting death-  
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic  
 CC activation which initiates the subsequent cascade of caspases  
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-  
 CC mediated apoptosis may have a role in the induction of peripheral  
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or  
 CC both (By similarity).  
 CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC -!- SIMILARITY: Contains 1 death domain.  
 CC  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:21 ; Search time 87.6712 Seconds  
(without alignments)  
921.313 Million cell updates/sec

Title: US-10-067-122B-2  
Perfect score: 1428  
Sequence: 1 MGNNCYNVWVILLVGCEK.....DACSCRCPOEEGGGGYEL 256

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1166.5	81.7	211	11 Q8R037	Q8R037 mus musculus
2	225	15.8	275	11 Q80WM9	Q80WM9 mus musculus
3	215.5	15.1	483	13 Q800K7	Q800K7 paralichthy
4	205	14.4	467	13 Q800I0	Q800I0 gallus gall
5	203.5	14.3	250	11 Q8C4K3	Q8C4K3 mus musculus
6	199	13.9	276	13 Q9DDD2	Q9DDD2 gallus gall
7	188	13.2	223	4 Q86YK5	Q86YK5 homo sapien
8	187	13.1	462	13 Q905B0	Q905B0 gallus gall
9	185.5	13.0	289	11 Q8K2X6	Q8K2X6 mus musculus
10	183.5	12.9	267	6 O02764	O02764 oryctolagus
11	182	12.7	459	11 Q62327	Q62327 mus musculus
12	180.5	12.7	457	4 Q8IVS6	Q8IVS6 homo sapien
13	180.5	12.6	482	11 Q88734	Q88734 mus musculus
14	180	12.6	651	13 Q98SM6	Q98SM6 gallus gall
15	176.5	12.4	283	6 Q9XSZ8	Q9XSZ8 cercopithec
16	176	12.3	285	13 Q90W71	Q90W71 oncorhynch

17	174.5	12.2	274	6 Q7YRL5	Q7YRL5 canis famil
18	173	12.1	167	12 Q9DJL2	Q9DJL2 cowpox viru
19	172.5	12.1	186	13 Q7ZZY5	Q7ZZY5 gallus gall
20	172	12.0	317	13 Q8JFV6	Q8JFV6 brachydanio
21	171.5	12.0	196	11 Q8VC17	Q8VC17 mus musculu
22	171	12.0	167	12 Q8UYL3	Q8UYL3 vaccinia vi
23	169	11.8	186	12 Q911R5	Q911R5 vaccinia vi
24	169	11.8	186	12 Q9WJB4	Q9WJB4 vaccinia vi
25	168	11.8	186	12 Q72735	Q72735 cowpox viru
26	168	11.8	285	13 Q90YS6	Q90YS6 oncorhynch
27	167.5	11.7	278	6 Q8SQ34	Q8SQ34 sus scrofa
28	165.5	11.6	302	13 Q9FUS0	Q9FUS0 salvelinus
29	163	11.4	186	12 Q9YP87	Q9YP87 cowpox viru
30	161.5	11.3	401	13 Q9PRG7	Q9PRG7 xenopus lae
31	161	11.3	167	12 Q72762	Q72762 cowpox viru
32	160	11.2	433	11 Q91ZM6	Q91ZM6 rattus norv
33	158	11.1	474	11 Q80WY6	Q80WY6 rattus norv
34	155	10.9	277	6 Q8WMQ2	Q8WMQ2 ovis aries
35	154	10.8	318	13 Q7T2H3	Q7T2H3 oncorhynch
36	152	10.6	1792	13 Q57484	Q57484 gallus gall
37	151	10.6	169	11 Q9JKE0	Q9JKE0 rattus norv
38	151	10.6	235	13 Q8JFU6	Q8JFU6 brachydanio
39	149.5	10.5	1997	10 Q8LRM7	Q8LRM7 chlamydomon
40	146.5	10.3	573	11 Q8BZU6	Q8BZU6 mus musculu
41	145	10.2	438	13 Q9DFV0	Q9DFV0 brachydanio
42	144	10.1	349	12 Q57111	Q57111 variola vir
43	143	10.0	322	12 Q72761	Q72761 cowpox viru
44	142.5	10.0	645	5 Q97448	Q97448 giardia lam
45	142	9.9	347	12 Q57119	Q57119 cowpox viru

ALIGNMENTS

RESULT 1  
Q8R037 ID Q8R037 PRELIMINARY; PRT; 211 AA.  
AC Q8R037;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Similar to tumor necrosis factor receptor superfamily, member 9.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC028507; AAH28507.1; -;  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS01186; EGF 2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
KW Receptor.SQ SEQUENCE 211 AA; 22452 MW; 1EECA84EA32A8D50 CRC64;

Query Match 81.7%; Score 1166.5; DB 11; Length 211;  
Best Local Similarity 82.0%; Pred. No. 1e-111;  
Matches 210; Conservative 0; Mismatches 1; Indels 45; Gaps 1;

Qy	1	MGNNCYNVWVILLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSIGGQPN 60
Db	1	MGNNCYNVWVILLVGCEKVGAVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSIGGQPN 60
Qy	61	CNLCRVAGYFRFKFKFCSSTHNAECEIEGFHCLGPGQCTRCCKDCRPGQELTKQCKTCS 120
Db	61	CNLCRVAGYFRFKFKFCSSTHNAECEIEGFHCLGPGQCTRCCKDCRPGQELTKQCKTCS 120

QY 121 LGTENDONGTVCRTWNCNCSLDGRSVLKTGTTTEKDVVCGPPVSPSPSTTISVTPEGGPG 180  
 Db 121 LGTENDONGTVCRTWNCNCSLDGRSVLKTGTTTEKDVVCGPPVSPSPSTTISVTPEGGPA 180  
 QY 181 GHSLQVLTFLALTSALLLALIFITLLFSLVLRKPPHIFKQPPFKTTTGAQEEEDACS 240  
 Db 181 -----FKTTTGAQEEEDACS 195  
 QY 241 CRCQEEEGGGGYEL 256  
 Db 196 CRCQEEEGGGGYEL 211

RESULT 2

Q80WM9 PRELIMINARY; PRT; 275 AA.  
 ID Q80WM9  
 AC Q80WM9  
 DT 01-JUN-2003 (TREMELrel. 24, Created)  
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 14 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Thymus;  
 RA Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;  
 RT "Light regulation in a murine model of ovarian carcinoma."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY264405; AA089081.1;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR008063; Fas receptor.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR PRINTS; PR01680; FASRECEPTOR.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Signal.  
 FT SIGNAL 1 38 Potential.  
 SQ SEQUENCE 275 AA; 30171 MW; C4A7EAD8EFC0521D CRC64;

Query Match 15.8%; Score 225; DB 11; Length 275;  
 Best Local Similarity 26.2%; Pred. No. 7.7e-15;  
 Matches 73; Conservative 31; Mismatches 111; Indels 64; Gaps 13;  
 QY 3 NNCYNVVVIVLLVGCERKVGAV-----QNSCDNCQPG-----TFCKRY-NPVCKS 46  
 Db 18 DNTFRLVPCVFLNLLQRLISAQPSCRQEEFLVGDCECPMCNPGVHVQVCSEHTGVCAP 77  
 QY 47 CPPSTFSS-IGQPNCNICRVCA--AGYFRFKKFCSSSTHNAECEIEGFHCL---GPQCT 99  
 Db 78 CPPQTYTAHANGLSKLPCGVCDPDMGLLTWQE-CSSWKDTVCRCIPGYFCENQDGSCHS 136  
 QY 100 RC--EKDCRPGQELTKG-----CKTCSLGTFFNDQNGTVCRTWNCNCSLDGRSVLKTG 150  
 Db 137 TCLQHTTCPPGQVRKRGTHDQDTCVADCLTGTFLGGTQEECLPWTNCSAFQGEV-RRG 195  
 QY 151 TTEKDVVCGPPVSPSPSTTISVTPEGGGHSQVLTFLALTSALLLALIFITLLFSV 210  
 Db 196 TNSTDFTCSSQVYVVS-----ILLPLVIVGAGIAGFLICT----- 232  
 QY 211 LKWTIRKPPHIFKQPPFKTTTGAQEEEDACSRCRCQEEEG 249  
 Db 233 -----RLHTSSVAKELEPFQEQQENTIRFPVTEVG 264

RESULT 3

Q800K7 PRELIMINARY; PRT; 483 AA.  
 ID Q800K7  
 AC Q800K7  
 DT 01-JUN-2003 (TREMELrel. 24, Created)  
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Tumor necrosis factor receptor-2.  
 GN TNFR-2.  
 OS Paralicthys olivaceus (Flounder).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Pleuronectoidei; Paralicththyidae; Paralicththys.  
 OX NCBI\_TaxID=8255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Park C., Kurobe T., Hirono I., Aoki T.;  
 RT "Cloning and characterization of cDNAs for two distinct tumor necrosis  
 factor receptor superfamily genes from Japanese flounder Paralicththys  
 olivaceus."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB080947; BAC52226.1;  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 KW Receptor.  
 SQ SEQUENCE 483 AA; 52227 MW; EE55874A8C7F2085 CRC64;

Query Match 15.1%; Score 215.5; DB 13; Length 483;  
 Best Local Similarity 25.6%; Pred. No. 1.3e-13;  
 Matches 70; Conservative 31; Mismatches 93; Indels 79; Gaps 13;  
 QY 23 AVQNSCDNCQPGTFCRKYNPVCKSCPPSTFSSIGGQPNICRVCAGYFRFKFCSSSTHN 82  
 Db 57 ATESVCKQCDSGQYMEKNVYAKCL-----SCNCKSNKG-LQYAQRCSSTTR 103  
 QY 83 AECEIEGFHCL---GPQCTRCE--KDCRPGQELTKG-----CKTCSLGT-NDQN 128  
 Db 104 TGCVCCKPGVYCIIMDFNPNYCAECRNYSQCRAGYVSLPGKANSVKELCPDGMFSNTSS 163  
 QY 129 GTGVCRTWNCNCSLDGRSVLKTGTTTEKDVVVC-----GP----- 160  
 Db 164 NTETCRPHDTC--HGKAVVRKGNNTSDTVCCEGVAPSSLFQDITTKGHPGILFSTPTIR 221  
 QY 161 PWSFSPSTTISVT-----PEGPGGHSQVLTFLALTSALLLALIFI 204  
 Db 222 STVSATPDATLSVASVSDEVFTHTIKSPPPYKPPGGS---LAALIAGWGFILLFI 277  
 QY 205 TLLFSLVKWIRKPPHIFKQPPFKTTTGAQEEED 237  
 Db 278 ILVF-LCKAVRSKDVPTF-QPKVDANGNCESDD 308

RESULT 4

Q800IO PRELIMINARY; PRT; 467 AA.  
 ID Q800IO  
 AC Q800IO  
 DT 01-JUN-2003 (TREMELrel. 24, Created)  
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE CD30 protein precursor.  
 GN CD30.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]

RP SEQUENCE FROM N.A.  
RA Burgess S.C.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RA SEQUENCE FROM N.A.  
RA Burgess S.C.;  
RL Thesis (1998), Bristol University, U.K.  
DR EMBL; AJ276964; CAC79223.1; --  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
KW Signal.  
FT SIGNAL  
FT CHAIN  
SQ SEQUENCE 467 AA; 51350 MW; F9AD4F77DEEC8588 CRC64;  
  
Query Match 14.4%; Score 205; DB 13; Length 467;  
Best Local Similarity 24.4%; Pred. No. 1.5e-12;  
Matches 69; Conservative 36; Mismatches 116; Indels 62; Gaps 10;  
  
QY 28 CDNCQPGTFCRKYNP-----CKSCPSTFSSIGQPNQNICRVAGYFRF--KKFCSST 80  
Db 49 CYQCPGVAKKKSCPMDDPDEDCMRGPEQYLNQSPKPRCDACVLCTKEFDLVEKAPCSFN 108  
QY 81 HNAECEIEGFHC---LGPQCTRCED--CRPGQELTKQ-----CKTCSLGTFTNDQ- 127  
Db 109 SSRVCECRPGMFCQTAANKTCMRQCRHTACKPGFGVKIRGTSETDVSCECPGTFSDQS 168  
QY 128 NGTGVRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSF----- 165  
Db 169 SSTDVCKPHTDCAKLNKVAQKGNATHDQVCTDQLPSYLTPTDTSIRITNETDSDVLKR 228  
QY 166 --SPSTTSV-----TPEGPGGHSLSQVLTFLALTSALLLALIFITLLFSVL----- 211  
Db 229 NANPVTLASILSSATTEIPGSTPEEEALAGTSPTLAKGETTTTTRGLVFWAVLSVMVLPVG 288  
QY 212 -----KW-IRKKFPHFQPFKKTGAAQEEEDACSCRCPQEE 248  
Db 289 MLSFWQWVKCKRIFILKQKRSDLVDVKYAKITLTDTKCPPEEE 331  
  
RESULT 5  
Q8C4K3 PRELIMINARY; PRT; 250 AA.  
AC Q8C4K3;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Tumor necrosis factor receptor superfamily.  
GN TNFRSF18.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RA SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
DR EMBL; AK081878; BAC38357.1; --  
DR MGD; MGI:894675; Tnfrsf18.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR SMART; SM00208; TNFR; 2.  
SQ SEQUENCE 250 AA; 27814 MW; 6963E94F414C16B4 CRC64;

Query Match 14.3%; Score 203.5; DB 11; Length 250;  
Best Local Similarity 29.8%; Pred. No. 1.1e-12;  
Matches 64; Conservative 26; Mismatches 84; Indels 41; Gaps 10;  
  
QY 54 SIGGQPNQ-----NICRVAGYFRFKKFCSTHNAECECI-EGFHCCLGPQCTRCE 102  
Db 22 SVVEEPGGGPGKVQNGSGNTRCCSLYAPGKEDCP---KERCICVTPEYHCGDPQCKICK 78  
QY 103 K-DCRPGQELTKQ-----CKTCSLGTFTNDQNGTGVCRPWTNCSLDGRSVLKTGTTEK 154  
Db 79 HYPGQGVQGVESQDIVFGFRCVACAMGTFS-AGRDGHCLRLWNTNCSQGFELTMFPNGKTH 137  
QY 155 DVVCGPPVVSFSPSTTISVTPEGGPGHSLQVLTFLALTSALLLALIFITLLFSVLKWI 214  
Db 138 NAVCIP-----EPLPEQY-----GH-----LTVIFLWMAACIFFLTTVQLGLHIWQLR 181  
QY 215 RKKFPHFQPFKKTGAAQEEEDACSCRCPQEEBEG 249  
Db 182 RQHMCPRETQPFQAEVQLSA--EDACSFQFPPEERG 214  
  
RESULT 6  
Q9DDD2 PRELIMINARY; PRT; 276 AA.  
AC Q9DDD2;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Human CD40-homologue.  
GN TNFSF5.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RA SEQUENCE FROM N.A.  
RL Tregaskes C.A.;  
RL Thesis (2001), University of Reading, Reading, UNITED KINGDOM.  
DR EMBL; AJ293700; CAC20218.1; --  
DR HSSP; Q92956; 1JMA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR008063; Fas\_receptor.  
DR InterPro; IPR001005; Myb\_DNA\_binding.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00037; MYB\_1; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;  
  
Query Match 13.9%; Score 199; DB 13; Length 276;  
Best Local Similarity 24.6%; Pred. No. 3.6e-12;  
Matches 73; Conservative 40; Mismatches 96; Indels 88; Gaps 14;  
  
QY 10 VIVLLLVGCEKVGAVQN-----SCDNCQPG-----TFGR-KYNPVCKSCPSTFS 53  
Db 9 LLCALLLGGCGQPGDAVNCSDKQVEHKGRCNRCQPGKKLASECNDTDSVCTPCENGQYQ 68  
QY 54 -SIGGQPNQ-----NICRVAGYFRFKKFCSTHNAECECI-EGFHCCLGPQCTRCEKDCRPGQ 109  
Db 69 HSWTKERHCTPHEICEDNAGLI-VKRHGNATHNTVCQCRAGMHCHSDASCQTGVEN----- 122  
QY 110 ELTKQG-----CKTCSLGTFTNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153

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Db 123 EPCKQGFGEVAAABARMTPCEPCAEGTFSNVSSKTEPCHFWTSCEEKGLVVVKGTNT 182
QY 154 KDVVCGPPVWSPSPSTTISVTPEGPGHSLQVLTLFLALTSALLLALIFITLLFSVLKW 213
Db 183 SDVIC-----ESSRSSLSV-----LIPITAAVVTCLVGICLYCLVHTD 221
QY 214 IRKFFPHIFKQ-----PFXKTGAAQ-----EEDACSCRCPQEEE 248
Db 222 LRRGCP---KQAEABAPRELVTQPEEVPFVQBTLLGGQPVQAGEDGKESIAEQEQ 275

RESULT 7
Q86YK5
ID Q86YK5 PRELIMINARY; PRT; 223 AA.
AC Q86YK5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 (Fragment).
GN TNFRSF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Zeng Y.;
RT "Transcripts of CD40 isoform in peripheral mononuclear cells.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225405; AAO43990.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor.
FT NON TER
SQ SEQUENCE 223 AA; 24659 MW; 85C63C20BC4E0B1C CRC64;

Query Match 13.2%; Score 188; DB 4; Length 223;
Best Local Similarity 26.4%; Pred. No. 3.9e-11;
Matches 58; Conservative 31; Mismatches 87; Indels 44; Gaps 10;

QY 18 CEKVAGVQNS--CDNCQPG-----TFCKYNPV-CKSCPPSTF--SSIGQPNCNCRVCAG 69
Db 26 CREKQYLINSQCCSLCQPGQKLVSDCTETETELPCGESEFLDTWNRETHCHQHKYCDP 85
QY 70 Y--FRFKFCSSTHNAECEIEGFHCLGPQCTRC--EKDCRPG-----QELTKQGCKT 118
Db 86 NLGLRVQKGTSETDTICTCEEGWHTCTSEACESCVLHRS CSPGFGVQIATGVSDTICEP 145
QY 119 CSLGTF-NDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEG 177
Db 146 CPVGFENSVSSAFEKCHPWTSCETKDLVVQAGTKNTDVCVGPQ----- 189
QY 178 GPGGHSLOVLTFLALTSALLLALIFITLLFSVLKWK 217
Db 190 -DRLRALVVIPIIFGILFAILLVLVFI-----KKVAKK 221

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RESULT 8
Q805B0
ID Q805B0 PRELIMINARY; PRT; 462 AA.
AC Q805B0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-II.
GN TNFR-II.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayde A.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayed A., Horuchi H., Furusawa S., Matsuda H.;
RT "Molecular cloning and characterization of chicken Tumor necrosis
factor receptor-II (TNFR-II) and Tumor necrosis factor receptor
associated factor-5 (TRAF-5) genes.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB101004; BAC55966.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 462 AA; 50141 MW; 8B00A93305414782 CRC64;

Query Match 13.1%; Score 187; DB 13; Length 462;
Best Local Similarity 24.1%; Pred. No. 1.1e-10;
Matches 65; Conservative 36; Mismatches 117; Indels 52; Gaps 11;

QY 24 VQNSCDNCQPG-----TFCKYNPVCKSCPPSTFSSIGQ-PNCNCR-VCAGYFRFKKF 76
Db 43 LKKCCSKCPFGQKAECSHSDTKCLPLDPTTAVNRSPPQCFACSPPCRKGFVENQT 102
QY 77 CSSTHNAECEIEGFHCLGPQCTRC-----EKDCRPGQELTKQG-----CKTCSLGTF 124
Db 103 CTLSWDRICSCPPEYCLISMYQNCHICKVHKKGGRYVSRRTDSTDECKPCPPGTF 162
QY 125 NDQNGTGV-CRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPEGPGGHS 183
Db 163 SDEESYDTSCIPHTVC-----KSAVAGNNVNDTVCHDSVATALPHTAVNLPQSSTTNS 218
QY 184 LQVLT-----LFLALTSALLLALIFITL---LFSVLK-----WIRKKF 218
Db 219 GEIITQPVILNFVPDMSYIIGSVTGFLLVLIIVLGYCLFSKKALAYSQPTGAVDSPF 278
QY 219 PHIFKQPFKKTGAQEEEDACSCRCPQEEE 248
Db 279 SPTEKQCDKKVRNAGSQNSSSS---EQEEQ 305

RESULT 9
Q8K2X6
ID Q8K2X6 PRELIMINARY; PRT; 289 AA.
AC Q8K2X6;

```

DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to tumor necrosis factor receptor superfamily, member 5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC029254; AAH29254.1; --  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0005840; C:ribosome; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0006412; P:protein biosynthesis; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR008063; F: Fas receptor.  
DR InterPro; IPR001005; Myb\_DNA binding.  
DR InterPro; IPR001865; Ribosomal\_S2.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00037; MYB\_1; 1.  
DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 4.  
KW Receptor.  
SQ SEQUENCE 289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;

Query Match 13.0%; Score 185.5; DB 11; Length 289;  
Best Local Similarity 25.1%; Pred. No. 9.3e-11;  
Matches 61; Conservative 33; Mismatches 88; Indels 61; Gaps 11;  
QY 28 CDNCQPGTECRKY-----NPVCKSCPPSTFSSIGGQP-NCNCRVCAGY--FRFKKFCSS 79  
Db 38 CDLCQPGSRLTSHCTALEKTOCHPCDSGEFFSAQWNRETRCHQHRHCEPNQGLRVKKEGTA 97  
QY 80 THNAECIEGFHCLGPOCTRCEK--DCRPG-----QELTKQCKTCSLGTENDQNGT 130  
Db 98 ESDTVACKEGQHCTSKDCEACAOHTPCIPGFGVMEMATETTTDVTCHPCPVGFFSNQSSL 157  
QY 131 -GVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVWSPFSTTISVTPPEGGGHSLQVLTL 189  
Db 158 FEKCPWTSCEDKNLEVLQKGTSTQTNVICG-----L 188  
QY 190 FLALTSALLALI--FITLLFSVLKWKRPKPPHIFKQPKK--TTGAAQEEEDACSCRCPO 245  
Db 189 KSRMRALLVTPVVMGILITIFGVFLYIKK---VVKPKDNEILPPAARRQD-----PQ 238  
QY 246 EEE 248  
Db 239 EWE 241

RESULT 10  
O02764  
ID O02764 PRELIMINARY; PRT; 267 AA.  
AC O02764;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE OX40 precursor (Fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Chbb:HM;  
RA Isono T., Seto A.;  
RT "Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed T cell lines."  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB003911; BAA20059.1; --  
DR HSSP; Q92956; 1JMA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
KW Signal.  
FT NON TER 1 1  
FT SIGNAL <1 18 POTENTIAL.  
FT CHAIN 19 267 OX40.  
SQ SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;  
Query Match 12.9%; Score 183.5; DB 6; Length 267;  
Best Local Similarity 27.8%; Pred. No. 1.4e-10;  
Matches 77; Conservative 22; Mismatches 103; Indels 75; Gaps 17;  
QY 9 VVIVLLVCEK---VGAV---QNSCDNCQPG---TFC-RKYNPVCKSCPPSTFSSI 55  
Db 10 LLLGLLLGAEPRPDCVGTYPGGDRCCLECPGPGYGMVSRNCRNSQDTICHPCPEGFYNEA 69  
QY 56 GGQPNCNICRVACGYFRFKKFCSSSTHNAECIEGFHCLGPOCTRCEKDCRPG-QELT-- 112  
Db 70 VNYQACKPCTQC-----NRRSGSEPPQECT---HTRDTVCR-----CRPGTQPLNGY 113  
QY 113 KQG--CKTCSLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVC----- 158  
Db 114 KHGVDCAPCPQGHFSEGNR-ACRPWTNCTLAGKRTLQPASSISDAVCEDRSSLATQPWE 172  
QY 159 -----GPPVVSFS-----PSTTISVTPPEGGGHSLQVLTLFLALTSALLALIF 203  
Db 173 TPSAPYRPPTARTSTAWPRTAQGPSTP---TLEASKGPQLAIVLSIGLGLALLAAL- 228  
QY 204 ITLLFSVLKWKRP--HIFKQPKKTTGAAQEEEDA 238  
Db 229 LALYLHQRARPPKLPGGGSFRTP-----QEEQA 258

RESULT 11  
Q62327  
ID Q62327 PRELIMINARY; PRT; 459 AA.  
AC Q62327;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Murine tumour necrosis factor receptor 2 protein (fragment).  
GN TNFRSF1B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD;  
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;  
RT "Amino acid variation in the tumor necrosis factor receptor 2 is linked to autoimmune diabetes in NOD mice."  
RL Genomics 0:0-0(0).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD;  
RX MEDLINE=95178848; PubMed=7873884;  
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;  
RT "Allelic variation of the type 2 tumor necrosis factor receptor

RT Gene.;  
RL Mamm. Genome 5:726-727(1994).  
DR EMBL; X76401; CAA53981.1; -.  
DR PIR; I48854; I48854.  
DR HSSP; P19438; INCF.  
DR MGD; MGI:131483; Tnfirflb.  
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.  
DR GO; GO:0006954; P:inflammatory response; IMP.  
DR GO; GO:0008220; P:necrosis; IMP.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00505; TNFR\_NGFR\_2; 3.  
KW Receptor.  
FT NON TER 1 1 S -> T.  
FT VARIANT 87 87 T -> I.  
FT VARIANT 93 93 F -> I.  
FT VARIANT 268 268 S -> F.  
FT VARIANT 345 345 Y -> C.  
FT VARIANT 421 421  
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;  
Query Match 12.7%; Score 182; DB 11; Length 459;  
Best Local Similarity 26.6%; Pred. No. 3.5e-10;  
Matches 76; Conservative 25; Mismatches 109; Indels 76; Gaps 15;  
QY 25 QNSCDNCQPGT----FCRK-YNPVCKSCPSTFSSIGGQ-PNCNIC-RVCAGYFRFKFC 77  
Db 37 QMCCAKCPGQVGVGHFNKTSDTVCADCEASMYTQVWQFRTCLSCSSCSTDQVEIRAC 96  
QY 78 SSTHNAECECEIEGFHCL-----GPOCTFCEKDCRPGQELTKQG-----CKTCSLGT 123  
Db 97 TKQNRVCAACEAGRYCALKTHSGCRQCVFLSK-CGPGFGVASSRAPNGNVLCKACAPGT 155  
QY 124 FND-QNGTGVCPRWTNCSLDGRSVLKTGTETKDVVCGP--PWVSFSPSTTISVTP----- 175  
Db 156 FSDTTSSTDVCRPHRISCI---LAIPGNASTDCAVCAPEPTLSAIPRTLYVSQPEPTRS 211  
QY 176 -----EGGP-----GGHSLQVLTFLALTSALLLALIFITLIFS 209  
Db 212 QPLDQEPGSPQTPSILTSLSGSTPIIEQSTKGGISLPI-GLIVGVTs---LGLMLGLVNC 267  
QY 210 VLKWKIRKPFHIFKQPFKKTGTAAQEEDACSCRCQPEEGGGGYE 255  
Db 268 FILVQRKKP-----SCLQRDAKVHPVDEKSDAVGLE 301  
RESULT 12  
Q8IVS6  
ID Q8IVS6 PRELIMINARY; PRT; 457 AA.  
AC Q8IVS6;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Similar to tumor necrosis factor receptor superfamily, member 1B (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RA Strausberg R.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC042167; AAH42167.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00505; TNFR\_NGFR\_2; 2.

KW Receptor.  
FT NON TER 1 1  
SQ SEQUENCE 457 AA; 48120 MW; 1B634BBF1F5D77AC CRC64;  
Query Match 12.7%; Score 181; DB 4; Length 457;  
Best Local Similarity 25.4%; Pred. No. 4.4e-10;  
Matches 71; Conservative 36; Mismatches 102; Indels 70; Gaps 15;  
QY 20 KVGAVQNSCDNCQPG----TFCRK-YNPVCKSCPSTFSSI-GGQPNCNIC-RVCAGYFR 72  
Db 42 RTGALGCGARLARPGQAHKVFCTKTSITVCDSCEDSTYTQLWNWVPECLSCSRCSDDQV 101  
QY 73 FKXFCSSSTHNAECEIEGFHC-LGPQ--CTRCE--KDCRPGQELTKQG-----CKTCS 120  
Db 102 ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLKRKCRPGFGVARPGTETSDVVCPCA 161  
QY 121 LGTF-NDQNGTGVCPRWTNCSLDGRSVLKTGTETKDVVC----- 158  
Db 162 PGTFSTNTSSDIDCRPHQICNV---VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQVVS 217  
QY 159 -----GPPVVSFSPSTTI-----SVTPEGGPGHSLQVLTFLALTSALLLALIFIT 205  
Db 218 TRSQHTQPTPEPSTAPSTSFLLPMGPPSPPAEGSTGDFALPV-GLIVGTALGLLIIGVVN 276  
QY 206 LLFSVLKWIRK-----KPPHIFKQPFKKTGTAAQE 235  
Db 277 CV--IMTQVKKKPLCLQREAKVPHLPADKARGTQGPQQ 313  
RESULT 13  
O88734  
ID O88734 PRELIMINARY; PRT; 482 AA.  
AC O88734;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE P80 TNF-alpha receptor.  
GN TNFR2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98414512; PubMed=9740674;  
RA Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;  
RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure and Characterization of the two Transcripts."  
RL Genomics 52:79-98(1998).  
DR EMBL; Y14619; CAA74969.1; -.  
DR EMBL; Y14620; CAA74969.1; JOINED.  
DR EMBL; Y14621; CAA74969.1; JOINED.  
DR EMBL; Y14622; CAA74969.1; JOINED.  
DR EMBL; Y14623; CAA74969.1; JOINED.  
DR EMBL; Y14679; CAA74969.1; JOINED.  
DR HSSP; Q92956; IJMA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00505; TNFR\_NGFR\_2; 3.  
KW Receptor.  
SQ SEQUENCE 482 AA; 51106 MW; F6CL5046B48FF83C CRC64;  
Query Match 12.6%; Score 180.5; DB 11; Length 482;  
Best Local Similarity 25.6%; Pred. No. 5.2e-10;  
Matches 75; Conservative 25; Mismatches 110; Indels 83; Gaps 14;  
QY 25 QNSCDNCQPG-----TFCRKYNPVCKSCPSTFSSIGGQ-PNCNIC-RVCAGY 70  
Db 52 QMCCAKCPGQVGVGHFNKTSDTVCADSDTVCADEASMYTQVWQFRTCLSCSSCSTD 111

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QY 71 FRFKFCSSTHNAECEIEGFHCL-----GPQCTRCEKDCRPGQELTKQG-----C 116
Db 112 QVETRACTKQQRVCAACEAGRYCALKTHSGSCRCQMLSK-CGPGFGVASSRAPNGNVL 170
QY 117 KTCSLGTEND-QNGTGVCRPWTNCSLDGRSVLKTGTTEKDVVCGP--PVVSFSPSTTISV 173
Db 171 KACAPGTFSDTTSSTDCVRPHRCSI-----LAIPGNASTDAVCAPESPTLSAIPRTLYVS 226
QY 174 TP-----EGGP-----GGHSLQVLTLFLALTSALLALI 202
Db 227 QPEPRSQPLDQEPGSPQTPSILTSLSGSTPIIBQSTKGISLPI-GLIVGVT--LGLL 282
QY 203 FITLLFVLKWKRPKPHIFKQPFKTTGAAQBEDACSCRCPOEEGGGGYE 255
Db 283 MLGLVNCFILVQRKKP-----SCLORDAKVPHVPDEKSDAVGLE 323

RESULT 14
Q98SM6
ID Q98SM6 PRELIMINARY; PRT; 651 AA.
AC Q98SM6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Death receptor 6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.2; -.
DR PIR; JC7705; JC7705.
DR HSSP; P19438; INCF.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;

Query Match 12.6%; Score 180; DB 13; Length 651;
Best Local Similarity 30.6%; Pred. No. 8.1e-10;
Matches 49; Conservative 22; Mismatches 71; Indels 18; Gaps 7;

QY 28 CDNCQPGTFCKKNP-----VCKSCPPSPFSS-IGGQPNICR-VCAGYFRFKKFSST 80
Db 52 CDKCPAGTYVSKHCTKSTLRCSPCPDGTFTHKENGIERCHPCRPKPCELPMIEKTHCTAL 111
QY 81 HNAECEIEGFHCLGPQCTRCEKDCRPGQELTKQG-----CKTCSLGTEND-QNGTGV 132
Db 112 TDRECTCLSGTFQINDTCVPTV-CPVGGVGRKKGTETEDVRCKPCLRGTFSDVPSSVMK 170
QY 133 CRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTIS 172
Db 171 CKTYTDCFGKNMVVVKPGTKESDNVCGSP--ASLPNTSLT 208

RESULT 15
Q9XSZ8
ID Q9XSZ8 PRELIMINARY; PRT; 283 AA.
AC Q9XSZ8;
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DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HVEAS.
GN HVEAS.
OS Cercopithecus aethiops (Green monkey) (GriVet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99296730; PubMed=10366573;
RA Foster T.P., Chouljenko V.N., Kousoulas K.G.;
RT "Functional characterization of the HveA homolog specified by African
RT green monkey kidney cells with a herpes simplex virus expressing the
RT green fluorescence protein.";
RL Virology 258:365-374(1999).
DR EMBL; AF147720; AAD37381.1; -.
DR HSSP; Q92956; IJMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;

Query Match 12.4%; Score 176.5; DB 6; Length 283;
Best Local Similarity 24.0%; Pred. No. 7.6e-10;
Matches 66; Conservative 32; Mismatches 100; Indels 77; Gaps 12;

QY 1 MGNNCYNVVIVLLLVGCEK---VGAVQNSCDNCQPGTFCR----KYNPVCKSCPPST 51
Db 30 LGSSCY-----APALPSCKEDEYVGS--ECCPKCGPGHVRQACGEQTGVCEPCSPGT 82
QY 52 F-SSIGGQPNICRVC--AGYFRFKKFCSSSTHNAECEIEGFHCL---GPQCTRCE--K 103
Db 83 YIAHFNGLSKLCQCMCDPAMGLRTSRNCSTANALCGSPGHFCCIQQGDHCAACRAYA 142
QY 104 DCRPGQELTKQG-----CKTCSLGTENDQNGTGVCRPWTNCSLDGRSVLKTGTTEKDV 156
Db 143 TSSPGQVRVQGGTESQDTLCQNCPPGTFSSNGTLEECQHGNKCSK----- 187
QY 157 VCGPPVVSFSPSTTISVTPEGPGGHSLQVLTFL--ALFSAALLALIFITLLFSLVKWI 214
Db 188 -----WLVTEAGPGTSSSRWYVWLLSGSLIVIVVGLIILRLIICVKR-- 230
QY 215 RKKFPFHIFKQPFKKTGAAQAEEDACSCRCPOEEEG 249
Db 231 -----RKSRGDVVKVIVSVQKRQAEAG 253

RESULT 16
Q90W71
ID Q90W71 PRELIMINARY; PRT; 285 AA.
AC Q90W71;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
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OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bringham J.T., Johnson A.L.;  
RT "Dcr3 expression in the hen."  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY251406; AAP03889.1; -  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS01186; EGF 2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
KW Receptor.  
FT NON\_TER 186 186  
SQ SEQUENCE 186 AA; 20671 MW; 31D65731DACB758E CRC64;  
  
Query Match 12.1%; Score 172.5; DB 13; Length 186;  
Best Local Similarity 28.8%; Pred. No. 1.3e-09;  
Matches 46; Conservative 23; Mismatches 66; Indels 25; Gaps 8;  
  
QY 9 VVIVLLVGCVKVAVQ-----NSCDNCQPGTF---CRKYNP-VCKSCPPSPSS 54  
Db 20 LLLLALGSSPPTYQWRDAGTKERVTCQCPPTGTFVAGHCTKERPTVCAPCPDLHYTH 79  
  
QY 55 IGGO-PNCNICRYCAGYFRFK-KFCSSSTHNAECIEGFHGLGPOCTRCCKDCRPGQELT 112  
Db 80 YWNVLEKCLYCNVXGGERQVEVQOCNATHNRACQCQEGFHAEMEFVQV-HSEXPVSGVV 138  
  
QY 113 KQG-----CKTCSLGTG-NDQNGTGVCPRWNTCSLDGR 144  
Db 139 KLGSPSENTQCRACPRGFSFSSSSSTPCRAHQNCTQLGK 178  
  
RESULT 20  
Q8JFV6 PRELIMINARY; PRT; 317 AA.  
AC Q8JFV6;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE SI:d107D16.1 (Novel protein similar to vertebrate nerve growth factor receptor (NGFR)) (Fragment).  
GN SI:D107D16.1.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ramsay H.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL591671; CAD43421.1; -  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS01186; EGF 2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
FT NON\_TER 1 1  
FT NON\_TER 317 317  
SQ SEQUENCE 317 AA; 34446 MW; D9B7E1C70DAF92B CRC64;  
  
Query Match 12.0%; Score 172; DB 13; Length 317;  
Best Local Similarity 23.1%; Pred. No. 2.5e-09;  
Matches 65; Conservative 38; Mismatches 96; Indels 82; Gaps 14;  
  
QY 29 DNCQPGTFCRKYNPVCKSCPP-----STFS-SIGGQPNICRV 66

Db 15 EECESGSFTHS-GECCVQCPPEGVKEKCGATQTECQLDSETSATFSHTDKQVCTE 73  
QY 67 CAGYFRFKFCSSSTHNAECIEGF--HCLGPQCTRCCKDCRPGQ-----ELTKQG-CK 117  
Db 74 CTGLMRMQPTCTDSNDAECVCNYGFYFNVLSRRCEPCTV-CPLGQGVDMRCELNHDVTVE 132  
QY 118 TCSLGTFTNDQNGT-GVCRPWTNCSLDGRSVLKTGTTEKDVVCGPPVVSFSPSTTISVTPE 176  
Db 133 ECRDEYSDQENTMDPCNPECTICEEDTEILLRNCTPTEDALCHDPL---SPTYPTSTGDS 189  
QY 177 G-----GPG-----GHSLOVLTFLFLALTSALLLALIFITLLF 208  
Db 190 GSFDTDLDLWSPSPGDDATTPKSPSPHFIGRGLNENLPIYCSILAAVVVGL----- 242  
QY 209 SVLKWIRKFPPIFKQ--PFKKTGAAQEEEDACSCRCPOEE 247  
Db 243 --LAYI-----IFKRWNSCKQKQANNAATANTQTPSP 275  
  
RESULT 21  
Q8VC17 PRELIMINARY; PRT; 196 AA.  
AC Q8VC17;  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022125; AAH22125.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0006915; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR008063; Fas receptor.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
KW Hypothetical protein.  
FT NON\_TER 1 1  
SQ SEQUENCE 196 AA; 21555 MW; 2AB3FF8905E260E8 CRC64;  
  
Query Match 12.0%; Score 171.5; DB 11; Length 196;  
Best Local Similarity 27.2%; Pred. No. 1.7e-09;  
Matches 62; Conservative 22; Mismatches 87; Indels 57; Gaps 11;  
  
QY 35 TFCRKYNPVCKSCPPSTFSIGGQPNICRVACGYFRFKFCSSSTHNAECIEGFHCL 94  
Db 2 TYTAHANGLSKCLP-----CGVCDPDMGLLTWQE-CSSWKDTCRCIPGYFCE 48  
QY 95 ---GPOCTRC--EKDCRPPGOELTKQG-----CKTCSLGTFTNDQNGTGVCPRWNTCSLD 142  
Db 49 NQDGSCHCSTCLQHTTCTPQGVKRGTHDQDVTVCADCLTGTFLSGTQEECLPWTNCSAF 108  
QY 143 GRSVLKGTTEKDVVCGPPVVSFSPSTTISVTPEG-GPGGHSLOVLTFLFLALTSALLLAL 201  
Db 109 QQEV-RRGTNSTDTTSCSSQVYVYVILLPLVIVGVGIAG-----FLICRRHLHT- 158  
QY 202 IFITLLFSVLKWKIRKFPPIFKQPKKTTGAQOEEDACSCRCPOEEG 249  
Db 159 -----SSVAKEL-----EPFQ-----QEQQENTIRFPVTEVG 185

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RESULT 22
Q8UYL3 ID Q8UYL3 PRELIMINARY; PRT; 167 AA.
AC Q8UYL3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CrmE protein.
GN CRME.
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USSR;
RA Reading P.C., Khanna A., Smith G.L.;
RT "Vaccinia virus CrmE encodes a soluble and cell-surface tumor necrosis
factor receptor that contributes to virus virulence.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ315962; CAC83048.1; --
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR SEQUENCE 167 AA; 18510 MW; 3B4A0DA27FB797D CRC64;
SQ
Query Match 12.0%; Score 171; DB 12; Length 167;
Best Local Similarity 30.7%; Pred. No. 1.6e-09;
Matches 50; Conservative 22; Mismatches 57; Indels 34; Gaps 9;
QY 9 VVIVL-----LLVGCCKVGVAVQNS-----CDNCPGTF----CRKY-NPVCKSCPP 49
Db 4 VIIILGLIINTNSLSMKCEQGVSYNSQLKCKLCKPGTYSHRCDYSDTICGHCP 63
QY 50 STFSI-GGPNICRVACGYFRKKF-CSSTHNAECIEGFHCL-----GPQCTRCEK 103
Db 64 DTFTSIYNSPWCSCRGCGTNRVEVTPCTPTTNRICHCDNSYCLLKASDGNVCVTCAP 123
QY 104 DCRPGQELTKQG-----CKTCSLGTFFND-QNGTGVCRPWT 137
Db 124 KTKCGRGYKKGEDMGNTICKCRKGYSDIVSDSDQCKPMT 166
RESULT 23
Q911R5 ID Q911R5 PRELIMINARY; PRT; 186 AA.
AC Q911R5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumour necrosis family receptor.
GN A53R.
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USSR;
RA Reading P.C., Khanna A., Smith G.L.;
RT "Vaccinia virus encodes a soluble and cell surface tumour necrosis
factor receptor that contributes to viral virulence.";
RL Virology 0:0-0(0).
DR EMBL; AJ416893; CAC95181.2; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
QY 28 CDNCPGTFGR-----KYNPVCKSCPPSTFSSIGGQPN-CNICRVCA-GYFRFKKFCSS 80
Db 51 CNRCPGGEFAKVRGNGNDNTKCRCPHTYTAIPNYSNGCHQCRKCTGSGFD-KVKCTGT 109
QY 81 HNAECIEGFHCL--GPQCTRCEKDCRPGQE-----LTKQG---CKTCSLGTFFNDQ 127
Db 110 QNSKCSCLPGWYCATDSSQTEDC-RDCIPKRRCPCGYFGGIDEGQNPICKSCCVGEYCDY 168
QY 128 NGTGVCRPWTNCSL 141
Db 169 LRNYRLDPFPCKL 182
RESULT 24
Q9WJB4 ID Q9WJB4 PRELIMINARY; PRT; 186 AA.
AC Q9WJB4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumour necrosis factor receptor precursor.
GN A53R.
OS Vaccinia virus (strain Lister).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10252;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lister;
RX MEDLINE=99226947; PubMed=10211965;
RA Alcamì A., Khanna A., Paul N., Smith J.L.;
RT "Vaccinia virus strains Lister, USSR and Evans express soluble and
cell-surface tumour necrosis factor receptors.";
RL J. Gen. Virol. 80:949-959(1999).
DR EMBL; Y17728; CAB41042.1; --
DR HSSP; Q92956; LUMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR KW Receptor; Signal.
FT SIGNAL 1
SQ SEQUENCE 186 AA; 20646 MW; D83CD9180276EE31 CRC64;
Query Match 11.8%; Score 169; DB 12; Length 186;
Best Local Similarity 31.3%; Pred. No. 2.9e-09;
Matches 42; Conservative 21; Mismatches 49; Indels 22; Gaps 8;
QY 28 CDNCPGTFGR-----KYNPVCKSCPPSTFSSIGGQPN-CNICRVCA-GYFRFKKFCSS 80
Db 51 CNRCPGGEFAKVRGNGNDNTKCRCPHTYTAIPNYSNGCHQCRKCTGSGFD-KVKCTGT 109
QY 81 HNAECIEGFHCL--GPQCTRCEKDCRPGQE-----LTKQG---CKTCSLGTFFNDQ 127
Db 110 QNSKCSCLPGWYCATDSSQTEDC-RDCIPKRRCPCGYFGGIDEGQNPICKSCCVGEYCDY 168
QY 128 NGTGVCRPWTNCSL 141
Db 169 LRNYRLDPFPCKL 182
RESULT 24
Q9WJB4 ID Q9WJB4 PRELIMINARY; PRT; 186 AA.
AC Q9WJB4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tumour necrosis factor receptor precursor.
GN A53R.
OS Vaccinia virus (strain Lister).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10252;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lister;
RX MEDLINE=99226947; PubMed=10211965;
RA Alcamì A., Khanna A., Paul N., Smith J.L.;
RT "Vaccinia virus strains Lister, USSR and Evans express soluble and
cell-surface tumour necrosis factor receptors.";
RL J. Gen. Virol. 80:949-959(1999).
DR EMBL; Y17728; CAB41042.1; --
DR HSSP; Q92956; LUMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR KW Receptor; Signal.
FT SIGNAL 1
SQ SEQUENCE 186 AA; 20646 MW; D83CD9180276EE31 CRC64;
Query Match 11.8%; Score 169; DB 12; Length 186;
Best Local Similarity 31.3%; Pred. No. 2.9e-09;
Matches 42; Conservative 21; Mismatches 49; Indels 22; Gaps 8;
QY 28 CDNCPGTFGR-----KYNPVCKSCPPSTFSSIGGQPN-CNICRVCA-GYFRFKKFCSS 80
Db 51 CNRCPGGEFAKVRGNGNDNTKCRCPHTYTAIPNYSNGCHQCRKCTGSGFD-KVKCTGT 109
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QY 81 HNAECIEGFGHCL--GPOCTRCEKDCRPGQE-----LTKQG---CKTCSLGTENDQ 127  
Db 110 QNSKSCSLPGWYCATDSSQTEDC-RDCIPKRCPCGYFGGIDEQGNPICKSCCVGEYCDY 168  
QY 128 NGTGVCPRWTNCSL 141  
Db 169 LRNYRLDPFPCKL 182

RESULT 25.  
O72735 PRELIMINARY; PRT; 186 AA.  
AC O72735;  
DT 01-AUG-1998 (TReMBLrel. 07, Created)  
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE A56R protein.  
GN A56R.  
OS Cowpox virus (CPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10243;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GRI-90;  
RX MEDLINE=98229462; PubMed=9568042;  
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,  
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;  
RT "Species-specific differences in genome organization of cowpox,  
RT smallpox, and vaccinia viruses";  
RL Virology 243:432-460(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GRI-90;  
RX MEDLINE=97068532; PubMed=8963248;  
RA Saifonov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,  
RA Shchelkunov S.N., Sandakhchiev L.S.;  
RT "Genes of a circle of hosts for the cowpox virus";  
RL Dokl. Akad. Nauk 349:829-833(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GRI-90;  
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Miheev M.V.,  
RA Ryazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,  
RA Sandakhchiev L.S.;  
RT "Structure-function and organization of cowpox virus strain GRI-90  
RT complete genome";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GRI-90;  
RA Totmenin A.V.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X94355; CAD90723.1; --  
DR HSSP; Q92956; LJMA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_2; 2.  
SQ SEQUENCE 186 AA; 20482 MW; D2342F1040A00AE3 CRC64;

Query Match 11.8%; Score 168; DB 12; Length 186;  
Best Local Similarity 31.3%; Pred. No. 3.7e-09;  
Matches 42; Conservative 20; Mismatches 50; Indels 22; Gaps 8;  
QY 28 CDNCOPGTFCR-----KYNPVCKSCPPSTFFSIGGQPN-CNICRVC-AGYFRFKFCSST 80  
Db 51 CNQCPGFEFAKVRCSGSDNTKCECPHTYTAIPNYSNGCHQCRKCPCTGSD-KVKCTGT 109  
QY 81 HNAECIEGFGHCL--GPOCTRCEKDCRPGQE-----LTKQG---CKTCSLGTENDQ 127

Db 110 QNSKSCSLPGWYCATDSSQTEDC-RDCVPKSRPCGYFGGIDEQGNPICKSCCVGEYCDY 168  
QY 128 NGTGVCPRWTNCSL 141  
Db 169 LRNYRLDPFPCKL 182

RESULT 26  
O90YS6 PRELIMINARY; PRT; 285 AA.  
AC O90YS6;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE TNF decoy receptor.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liu L., Fujiki K., Dixon B., Sundick R.S.;  
RT "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine  
RT with a fractalkine-like stalk and a TNF decoy receptor using cDNA  
RT fragments containing AU-rich elements";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF401631; AAK91758.1; --  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00650; TNFR\_NGFR\_2; 1.  
KW Receptor.  
SQ SEQUENCE 285 AA; 31795 MW; SE3BD1B6EFC6BABC CRC64;

Query Match 11.8%; Score 168; DB 13; Length 285;  
Best Local Similarity 26.2%; Pred. No. 5.8e-09;  
Matches 58; Conservative 27; Mismatches 90; Indels 46; Gaps 12;  
QY 4 NCYNVWVILLVGCEKVGAVQN-----SCDNCQPGTFCRKY-----NPVC 44  
Db 6 NCFLLPLVFCGSGVPSVGAHTPTTYWRDDATGDSLTCDLCAPGYLLKHCTKDRKSDC 65  
QY 45 KSCPSTFSSIGGQ-PNCNIC-RVCAGYFRFKKFCSSSTHNAECECEGFCGLPQCTRCE 102  
Db 66 GPCPKSHVTEIWNVIERQYCNRFCTADEIESVPCQLHNRQCECKDGFYMTGHSR-H 124  
QY 103 KDCRPGQELTKQG-----CKTCSLGTEND-QNGTGVCPRWTNCSLGDGRSVLXTGTTEK 154  
Db 125 RRCPPGEGVISNGTAHTDVKCEPCPVGFSAVSSRRKACQKFSVCP-PGRTTI-PGNDMN 182  
QY 155 DWVCGPPVVSFSPSTTISVTPEGGP--GGH-----SLQVLT 188  
Db 183 DVYC-----SACRNGSRTHGQAICDGMELMEFLSLQILT 216

RESULT 27  
Q8SQ34 PRELIMINARY; PRT; 278 AA.  
AC Q8SQ34;  
DT 01-JUN-2002 (TReMBLrel. 21, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE CD40.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;

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RN
RP SEQUENCE FROM N.A.
RA West K.A., Li A.W., Rowden G.;
RT "Characterization of the Porcine CD40 Molecule.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF248545; AAL92924.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
SQ SEQUENCE 278 AA; 30951 MW; 20D446E44AF93DD2 CRC64;

Query Match 11.7%; Score 167.5; DB 6; Length 278;
Best Local Similarity 24.3%; Pred. No. 6.3e-09;
Matches 55; Conservative 24; Mismatches 64; Indels 83; Gaps 9;

QY 32 QPQTEFCR-----YNPVCKSCPSTFSSIGGQPCNIC-----RVCAGYFR 72
Db 21 EPTISCKENQYPTNSRCNLCPP-----GQKLVNHCTEVTETCLPCSSEFLATWNR 73
QY 73 FK-----KFC-----SSTHNAECIEGFHCLGPQCTRC--EKDCRPG----- 108
Db 74 EKCHQHKYCDNGLQVQREGTSKTDTTVCVSEGHCHTNSACESCTLHSLCFPLGLGVKQ 133
QY 109 --QELTKQCKTCSLGTFF--NDONGTGVCRPWTNCSLDGRSVLKTGTTTEKDVVCGPPVVSF 165
Db 134 MATEVSDTICEPCVGFNSVSSASEKQCPWTSCSKGLVEQVQAGTNKTDVWCG----- 187
QY 166 SPSTTISVTPEGGPGHSLQVLTFLALTSALLLALIFITLLFSVL 211
Db 188 -----FQSRMRALVVIPTILGILFAVL 209

RESULT 28
Q9PUS0
ID Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20111091; PubMed=10642582;
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation.";
RL Biol. Reprod. 62:420-426 (2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSSP; O14763; 1D4V.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.

SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 11.6%; Score 165.5; DB 13; Length 302;
Best Local Similarity 27.2%; Pred. No. 1.1e-08;
Matches 40; Conservative 20; Mismatches 70; Indels 17; Gaps 6;

QY 28 CDNCQGTFCR-----KYNPVCKSCPSTFSSIGGQ-PNCNICRVCAGYFRPKFCSSSTH 81
Db 36 CDRCPGTYLRAPCSAMRKSDCAECNPNGAYTEFWNHISKLCRCMCAENQVVKQECSPSN 95
QY 82 NAECECIEGFHCLGPQCTRC--EKDCRPGQELTKQ-----CKTCSLGTFFND-QNGTG 131
Db 96 NCECEKEGYF-FNKKYEACIKHKECPGPGYGANTTGTTPHQDTECVQCQAGFYSEVSSAKA 154
QY 132 VCRPWTNCSLDGRSVLKTGTTTEKDVVC 158
Db 155 TCLAQSNCKVGLRVVLKQDWHNTLC 181

RESULT 29
Q9YP87
ID Q9YP87 PRELIMINARY; PRT; 186 AA.
AC Q9YP87;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Soluble TNF receptor Crmc (VI83).
GN CrMC.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Redgene;
RA Smith C.A., Goodwin R.G., Pickup D.J.;
RT "Cowpox virus Encodes a second soluble TNF receptor (Crmc) Distinct
RT from Crmb.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=83117629; PubMed=6961398;
RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
RT repeated and unique sequence elements.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116 (1982).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=90177240; PubMed=2309453;
RA Parsons B.L., Pickup D.J.;
RT "Transcription of orthopoxvirus telomeres at late times during
RT infection.";
RL Virology 175:69-80 (1990).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=91196263; PubMed=2014645;
RA Hu F.Q., Pickup D.J.;
RT "Transcription of the terminal loop region of vaccinia virus DNA is
RT initiated from the telomere sequences directing DNA resolution.";
RL Virology 181:716-720 (1991).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton Red;
RX MEDLINE=94378510; PubMed=8091665;
RA Hu F.Q., Smith C.A., Pickup D.J.;
RT "Cowpox virus contains two copies of an early gene encoding a soluble
RT secreted form of the type II TNF receptor.";
RL Virology 204:343-356 (1994).
RN [6]
RP SEQUENCE FROM N.A.
```







```
Db 922 CPCDPGPGPRHFAASCYQDGRS-----RQVVC-----HCSPGYTGPRCDECAPGY 968
QY 181 GHSLO 185
Db 969 GDPLQ 973

RESULT 37
Q9JKE0
ID Q9JKE0 PRELIMINARY; PRT; 169 AA.
AC Q9JKE0;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE CD40 protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 62-169 FROM N.A.
RC STRAIN=Wistar; TISSUE=Smooth muscle;
RX MEDLINE=99330195; PubMed=10403401;
RA Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
RT "Cytokine-inducible CD40 gene expression in vascular smooth muscle
RT cells is mediated by nuclear factor kappaB and signal transducer and
RT activator of transcription-1."
RL FEBS Lett. 453:191-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Smooth muscle;
RA Krzesz R., Hecker M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Smooth muscle;
RA Gao D., Hecker M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Smooth muscle;
RA HSSP; Q92956; 1JMA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; F:as receptor.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00020; TNFR_C6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
FT NON_TER 169
SQ SEQUENCE 169 AA; 18525 MW; F199D91EFA224A26 CRC64;

Query Match
Best Local Similarity 10.6%; Score 151; DB 11; Length 169;
Matches 40; Conservative 17; Mismatches 53; Indels 22; Gaps 8;

QY 28 CDNCQPG-----TFCRKYNV-CSCPPSTFSSIGQP-NCNICRVCA--GYFRFKFCSS 79
Db 38 CDLCQPGNRLVSHCTALEKTQCQPCDSCGFSAHWNREIRCHQHRHCELNQLQVKEGTA 97
QY 80 THNAECEIEGFHCLGPQCTRC--EKDPRG-----QELTKQGKCTCSLGTNDQNGT 130
Db 98 VSDTVCTCKEGQHCASKECETCAQHRPCGPGFVGVQVQMATETTTDVCQPCPVGFSS--NGS 155

Query Match
Best Local Similarity 30.3%; Score 151; DB 11; Length 169;
Matches 40; Conservative 17; Mismatches 53; Indels 22; Gaps 8;

QY 28 CDNCQPG-----TFCRKYNV-CSCPPSTFSSIGQP-NCNICRVCA--GYFRFKFCSS 79
Db 38 CDLCQPGNRLVSHCTALEKTQCQPCDSCGFSAHWNREIRCHQHRHCELNQLQVKEGTA 97
QY 80 THNAECEIEGFHCLGPQCTRC--EKDPRG-----QELTKQGKCTCSLGTNDQNGT 130
Db 98 VSDTVCTCKEGQHCASKECETCAQHRPCGPGFVGVQVQMATETTTDVCQPCPVGFSS--NGS 155
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QY 131 GV---CRPWTNC 139
Db 156 SLFEKCHPWTSC 167

RESULT 38
Q8JFU6
ID Q8JFU6 PRELIMINARY; PRT; 235 AA.
AC Q8JFU6;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE SI:dz94E17.1 (Novel protein similar to nerve growth factor receptor
DE (NGFR)) (Fragment).
GN SI:dz94E17.1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL596203; CAD43457.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 1
FT NON_TER 235
SQ SEQUENCE 235 AA; 25783 MW; 7C6CA5FAFB16E7BE CRC64;

Query Match
Best Local Similarity 10.6%; Score 151; DB 13; Length 235;
Matches 58; Conservative 35; Mismatches 85; Indels 60; Gaps 12;

QY 51 TFS-SIGGQPNICRVCAGYFRFKKFCSSSTHNAECEIEGF--HCLGPQCTRCCKDCRP 107
Db 2 TFSATFSDTKQCVCTECTGLMRMQTPCTDSNDACVGVNVLSSRCEPCTV-CPL 60
QY 108 GQ-----ELTKQG-CKTCSLGTNDQNGT-GVCRPWTNCSLDGRSVLKTGTTEKDVVCG 159
Db 61 GQGVDMRCELNHDVTCECRDETYSDQNTMDPCMPCTICEEDTEILLRNCTPTEDALCH 120
QY 160 PPWVSFSPSTISVTPEG-----GPG-----GHSLOVLTFL 191
Db 121 DPL---SPTYPTSTGDSGSFDTDLRLWSPSPGDDATPKPSSPHFGRGLNENLIPIYC 177
QY 192 ALTSALLALIFITLLFSLVKWIRKFFPHFKQ--PFKKTGAQAEEDACSCRCQPEE 247
Db 178 SILAAVVVGL-----LAYI-----IFKRWNSCKONKQANNAATANQTPSPE 220

RESULT 39
Q8LRM7
ID Q8LRM7 PRELIMINARY; PRT; 1997 AA.
AC Q8LRM7;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mastigoneme-like protein.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
```

RP SEQUENCE FROM N.A.  
RA Song L.; Dentler W.L.;  
RT "Molecular cloning and characterization of a 240 kDa flagellar protein  
in Chlamydomonas";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF508983; AAM33552.1; --  
DR GO; GO:0004289; F:subtilase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000209; Peptidase S8.  
DR PROSITE; PS00136; SUBTILASE\_ASP; 1.  
SQ SEQUENCE 1997 AA; 206459 MW; A4061C41FEAA7047 CRC64;  
  
Query Match 10.5%; Score 149.5; DB 10; Length 1997;  
Best Local Similarity 26.5%; Pred. No. 3.7e-06;  
Matches 53; Conservative 24; Mismatches 64; Indels 59; Gaps 12;  
  
QY 28 CDNCPGTFCKYN-PVCKSCPSTFSSIGGQPNICR-----VCA----- 68  
Db 1603 CYTCQTGTENDEFSPQVCKACWSGSFASKRGLPTCEIAQPGFTFNVAANAATNTATLI 1662  
  
QY 69 -----GYFRFKKFCSSSTHNAEC-ECIEGFHCLGPQCTRCCKCRPGQ-- 109  
Db 1663 PTGLVKAQAAPTCCGMGYFQ-----SSAETTCTACAGVTYADQAGLAAC-KPCOPGRYQ 1716  
  
QY 110 -ELTKGCKTCSLGTENDONGTGVCPWPWNCSLDGRSVLKTGTTKDWVCGPPVVSF--- 165  
Db 1717 NSIGQRVCKPCDMGTYSRYGGE-LC---TKCPA-GTVASKTSSQ----CTPCAAGFYAN 1767  
  
QY 166 --SPSTTISVTPEGGPGGHS 183  
Db 1768 APDSATSCRACPRGYGYS 1787

RESULT 40  
Q8BZU6 PRELIMINARY; PRT; 573 AA.  
ID Q8BZU6  
AC Q8BZU6;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Death receptor 6.  
GN TNFRSF21 OR AA959878.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Colon;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
DR EMBL; AK033529; BAC28342.1; --  
DR MGD; MGI:2151075; Tnfrsf21.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS50017; DEATH DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
SQ SEQUENCE 573 AA; 63506 MW; BC883B4EC8F2FE94 CRC64;

Query Match 10.3%; Score 146.5; DB 11; Length 573;  
Best Local Similarity 29.9%; Pred. No. 2e-06;  
Matches 50; Conservative 18; Mismatches 64; Indels 35; Gaps 9;

QY 43 VKSCPSTFS-SICGQPNIC-RVCAGYFRFKKFCSSSTHNAECIEGFHCLGPQCTR 100  
Db 5 VCSSCPAGTFTTRHENGIERCHDCSQPCPWPMIERLPAAALTDREICPPGMYQSNGTGAP 64  
  
QY 101 CEKDCRPGQELTKQ-----CKTCSLGTEND-QNGTGVCRPWTNCSLDGRSVLKTGTT 152  
Db 65 -HTVCPVGVGVRKKGTENEDVRCKQCARGTFSDFSSVMKCKAHTDCLGQNLNVKPGTK 123  
  
QY 153 EKDVVCG-----PP---VVSFS-----PSTTISVTPEG 177  
Db 124 ETDNVCGMRLFFSSTNPPSSGTVTFSHPEHMHSHDVPSPTYE--PQG 168

Search completed: May 5, 2004, 14:40:33  
Job time : 89.6712 secs



GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:20 ; Search time 5.46233 Seconds

(without alignments)

568.992 Million cell updates/sec

Title: US-10-067-122B-2\_COPY\_105\_115

Perfect score: 62

Sequence: 1 CRPGQLTKQG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	62	100.0	11	7	ADC25950	Adc25950 Murine re
2	62	100.0	191	4	AAB66986	Aab66986 4lbb prot
3	62	100.0	256	2	AAR64199	Aar64199 Murine 4-
4	62	100.0	256	2	AAR70978	Aar70978 4-1BB rec
5	62	100.0	256	2	AAW04173	Aaw04173 Mouse rec
6	62	100.0	256	2	AAW26659	Aaw26659 Mouse 4-1
7	62	100.0	256	2	AAY28687	Aay28687 Mouse Rec
8	62	100.0	256	2	AAY33215	Aay33215 Murine CD
9	62	100.0	256	5	AAE22581	Aae22581 Mouse rec
10	62	100.0	256	5	ABB75954	Abb75954 Murine cy
11	62	100.0	256	7	ADC25939	Adc25939 Murine re
12	62	100.0	256	7	ADE87549	Ade87549 Mouse rec
13	57	91.9	12	5	AAE22582	Aae22582 Mouse rec
14	57	91.9	12	7	ADC25944	Adc25944 Murine re
15	50	80.6	255	2	AAR74087	Aar74087 Human rec
16	47	75.8	132	3	AAW94714	Aay94714 Tumour ne
17	47	75.8	219	2	AAW31759	Aaw31759 A novel h
18	47	75.8	219	2	AAW92523	Aaw92523 Human h4-
19	47	75.8	219	2	AAW92524	Aaw92524 Human h4-
20	47	75.8	219	4	AAE08545	Aae08545 Human h4-
21	47	75.8	219	6	ABB84639	Abb84639 Human h4-
22	47	75.8	255	2	AAR64197	Aar64197 Human 4-1
23	47	75.8	255	2	AAR70977	Aar70977 H4-1BB re
24	47	75.8	255	2	AAW04174	Aaw04174 Human rec
25	47	75.8	255	2	AAW26658	Aaw26658 Human 4-1

26	47	75.8	255	2	AAAY28688	Aay28688 Human rec
27	47	75.8	255	2	AAAY33214	Aay33214 Human CD1
28	47	75.8	255	4	AAE08546	Aae08546 Human h4-
29	47	75.8	255	4	AAB50521	Aab50521 Human tum
30	47	75.8	255	5	ABB75955	Abb75955 Human cyt
31	47	75.8	255	6	ABR39863	Abr39863 Human MOC
32	47	75.8	255	6	ABB84640	Abb84640 Human h4-
33	47	75.8	255	7	AAE39531	Aae39531 Human pro
34	47	75.8	255	7	ADC78803	Adc78803 Human PRO
35	47	75.8	255	7	ADD25599	Add25599 Binding d
36	47	75.8	255	7	ADE87541	Ade87541 Unknown h
37	43	69.4	265	6	AAE29933	Aae29933 Human LP2
38	43	69.4	389	4	AAU02951	Aau02951 Angiotens
39	43	69.4	845	5	AAG68259	Aag68259 Human POL
40	43	69.4	845	6	ABU12092	Abu12092 Novel hum
41	43	69.4	845	7	AAE38807	Aae38807 Human POL
42	43	69.4	880	7	ADB64680	Adb64680 Human pro
43	43	69.4	897	4	AAG65887	Aag65887 Amino aci
44	43	69.4	897	4	ABG06309	Abg06309 Novel hum
45	43	69.4	897	5	ABG91402	Abg91402 Primate L

ALIGNMENTS

RESULT 1

ADC25950

ID ADC25950 standard; peptide; 11 AA.

XX

AC ADC25950;

XX

DT 18-DEC-2003 (first entry)

XX

DE Murine receptor 4-1BB peptide - residues 105-115.

XX

KW receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;

XX

OS cancer; murine; mouse.

XX

PN Mus musculus.

XX

PD US2003100745-A1.

XX

PF 29-MAY-2003.

XX

PF 04-FEB-2002; 2002US-00067122.

XX

PR 07-NOV-1988; 88US-00267577.

XX

PR 30-JUL-1992; 92US-00922996.

XX

PR 01-FEB-1993; 93US-00012269.

XX

PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX

PI Kwon BS;

XX

DR WPI; 2003-678138/64.

XX

PT New cDNA gene encoding receptor protein 4-1BB, useful for isolating

XX

PT similar DNA sequences, and the encoded polypeptide and an antibody to it,

XX

PT useful for identifying ligands, and for modulating immune cell activity.

XX

PS Disclosure; Page 22; 77pp; English.

XX

CC The invention relates to a novel cDNA gene encoding receptor protein 4-

XX

CC 1BB. The cDNA gene of the invention demonstrates immunostimulant

XX

CC activities and may be useful as a probe to isolate DNA sequences encoding

XX

CC for proteins similar to the receptor protein encoded by the DNA. The

XX

CC protein, its fragments and derivatives may be useful as a probe to

XX

CC isolate ligands to receptor protein 4-1BB, for stimulating proliferation

XX SQ Sequence 11 AA;  
Query Match 100.0%; Score 62; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0003;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 1 CRPGQELTKQG 11  
RESULT 2  
AAB66986  
ID AAB66986 standard; protein; 191 AA.  
XX AC AAB66986;  
XX DT 19-APR-2001 (first entry)  
XX DE 41bb protein.  
XX KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;  
XX KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
XX KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
XX KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
XX KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
XX KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;  
XX KW ischaemia; Parkinson's disease.  
XX OS Unidentified.  
XX PN WO200103719-A2.  
XX PD 18-JAN-2001.  
XX PF 07-JUL-2000; 2000WO-US018667.  
XX PR 09-JUL-1999; 99US-00350670.  
XX PR 09-DEC-1999; 99US-00457647.  
XX PA (AMGE-) AMGEN INC.  
XX PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;  
XX WPI; 2001-103031/11.  
XX PT Treating conditions leading to bone loss such as rheumatoid arthritis,  
XX PT multiple sclerosis and asthma, comprises administering an osteoprotegerin  
XX PT protein in conjunction with e.g. inhibitors of interleukin and tumor  
XX PT necrosis factor alpha.  
XX PS Disclosure; Fig 2; 316pp; English.  
XX CC The present invention relates to a method for treating conditions leading  
XX CC to bone loss. The method comprises administering a purified and isolated  
XX CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)  
XX CC in conjunction with other substances such as tumour necrosis factor-alpha  
XX CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE  
XX CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet  
XX CC activating factor (PAF) antagonists. The method is useful for treating  
XX CC conditions leading to bone loss such as rheumatoid arthritis, multiple  
XX CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
XX CC useful for treating inflammation, systemic lupus erythematosus (SLE) and  
XX CC graft-versus-host disease (GVHD). Other diseases that can be treated  
XX CC include acute pancreatitis, Alzheimer's disease, anorexia,  
XX CC atherosclerosis, coronary conditions (e.g. myocardial infarction),  
XX CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,  
XX CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
XX CC psoriasis and septic shock. The present sequence was used in a sequence  
XX CC homology comparison  
XX SQ Sequence 191 AA;

XX SQ Sequence 11 AA;  
Query Match 100.0%; Score 62; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 0.0055;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115  
RESULT 3  
AAR64199  
ID AAR64199 standard; protein; 256 AA.  
XX AC AAR64199;  
XX DT 25-MAR-2003 (revised)  
XX DT 08-AUG-1995 (first entry)  
XX DE Murine 4-1BB polypeptide.  
XX KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;  
XX KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.  
XX OS Mus musculus.  
XX PN WO9426290-A1.  
XX PD 24-NOV-1994.  
XX PF 06-MAY-1994; 94WO-US005036.  
XX PR 07-MAY-1993; 93US-00060843.  
XX PA (IMMV) IMMUNEX CORP.  
XX PI Goodwin RG, Smith CA, Alderson MR;  
XX WPI; 1995-022265/03.  
XX DR N-PSDB; AAQ75428.  
XX CC Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB  
XX CC to transduce signal.  
XX PS Example 1; Page 44-45; 65pp; English.  
XX CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75422)  
XX CC are useful in a pharmaceutical composition for stimulating the immune  
XX CC system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring  
XX CC mechanisms of T-cell activation, as they are expressed on T lymphocytes.  
XX CC 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation  
XX CC of primary T-cells during the derivation of clonal T-cell lines. It may  
XX CC also be used to stimulate proliferation of activated T-cells, used in  
XX CC therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 256 AA;  
Query Match 100.0%; Score 62; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115  
RESULT 4  
AAR70978  
ID AAR70978 standard; protein; 256 AA.  
XX AC AAR70978;  
XX DT 25-MAR-2003 (revised)

DT 16-OCT-1995 (first entry)  
XX  
DE 4-1BB receptor protein.  
XX  
KW 4-1BB; receptor protein; immunosuppressive; autoimmune disease;  
KW organ transplantation; cell membrane ligand.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= Sig\_peptide  
XX  
XX WO9507984-A1.  
XX  
XX 23-MAR-1995.  
XX  
XX 15-SEP-1994; 94WO-US010457.  
XX  
XX 16-SEP-1993; 93US-00122796.  
XX  
XX (INDV ) UNIV INDIANA FOUND.  
XX  
XX Kwon BS;  
XX  
XX WPI; 1995-131352/17.  
DR N-PSDB; AAQ86127.  
XX  
XX Novel cDNA encoding human receptor protein H4-1BB - useful to produce the  
PT protein which is used to treat autoimmune disease and facilitate organ  
PT transplantation.  
XX  
XX Disclosure; Fig 1; 36pp; English.  
XX  
XX cDNA encoding the human receptor protein H4-1BB (given in AAQ86126) was  
CC isolated using PCR primers based on the homologous mouse 4-1BB gene  
CC (AAQ86127) encoding mouse receptor protein (AAR70978). (Updated on 25-MAR  
CC -2003 to correct PN field.)  
XX  
XX Sequence 256 AA;  
SQ  
Query Match 100.0%; Score 62; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db |||||  
105 CRPGQELTKQG 115  
RESULT 5  
AAW04173  
ID AAW04173 standard; protein; 256 AA.  
XX  
AC AAW04173;  
XX  
DT 12-DEC-1996 (first entry)  
XX  
DE Mouse receptor 4-1BB.  
XX  
XX Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;  
KW immunostimulant; cancer; autoimmune disease; graft rejection; therapy.  
KW  
XX Mus sp.  
OS  
XX WO9629348-A1.  
PN  
XX 26-SEP-1996.  
PD  
XX 22-MAR-1996; 96WO-US003965.  
PF  
XX 23-MAR-1995; 95US-00409851.  
PR  
XX

(INDV ) UNIV INDIANA FOUND.  
PA  
XX Kwon BS, Kang C;  
PI  
XX WPI; 1996-443138/44.  
DR N-PSDB; AAT39541.  
DR  
XX  
XX Monoclonal antibody specific for human receptor protein 4-1BB - used to  
PT enhance proliferation and activation of T-cells for treatment of cancer  
PT and to inhibit specific ligand binding for treating autoimmune diseases.  
PT  
XX Disclosure; Page 32-34; 48pp; English.  
PS  
XX Novel murine receptor protein 4-1BB (AAW04173) has the potential to  
CC function as an accessory signaling molecule during T-cell activation and  
CC proliferation. It may represent a cell surface molecule involved in T-  
CC cell-APC interactions and may also act as a B-cell costimulator. It is  
CC structurally related to members of the nerve growth factor receptor  
CC superfamily. Its amino acid sequence was deduced from an isolated cDNA  
CC clone (see also AAT39541). A human homologue, H4-1BB (AAW04174), was  
CC identified and used to raise a monoclonal antibody useful in cancer and  
CC autoimmune disease therapy  
XX  
XX Sequence 256 AA;  
SQ  
Query Match 100.0%; Score 62; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db |||||  
105 CRPGQELTKQG 115  
RESULT 6  
AAW26659  
ID AAW26659 standard; protein; 256 AA.  
XX  
AC AAW26659;  
XX  
XX 25-MAR-2003 (revised)  
DT 25-FEB-1998 (first entry)  
XX  
DE Mouse 4-1BB receptor.  
XX  
XX 4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte; T cell;  
KW proliferation; immunostimulant.  
KW  
XX Mus musculus.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..23  
FT /label= Sig\_peptide  
FT  
XX US5674704-A.  
PN  
XX 07-OCT-1997.  
PD  
XX 06-MAY-1994; 94US-00236918.  
PF  
XX 07-MAY-1993; 93US-00060843.  
PR  
XX (IMMV ) IMMUNEX CORP.  
PA  
XX Alderson MR, Goodwin RG, Smith CA;  
XX  
XX WPI; 1997-502333/46.  
DR N-PSDB; AAT91027.  
XX  
XX DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell  
PT proliferation in vitro, and as research tools.  
PT  
XX Disclosure; Col 39-40; 32pp; English.  
PS

XX This protein comprises mouse 4-1BB, a member of the tumour necrosis  
CC factor receptor superfamily that is expressed on helper, suppressor and  
CC cytolytic T cells, as well as on mouse brain tissue. A novel claimed  
CC cytokine, designated 4-1BB ligand (4-1BB-L) has been identified, cloned  
CC and sequenced (see AAW26656) that binds to murine 4-1BB. 4-1BB-L,  
CC especially its soluble extracellular domain, can be used to stimulate T-  
CC cell proliferation in vitro, as a research tool and as an affinity ligand  
CC for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)  
XX

SQ Sequence 256 AA;

Query Match 100.0%; Score 62; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115

RESULT 7  
AAV28687  
ID AAV28687 standard; protein; 256 AA.  
XX  
AC AAV28687;  
XX

DT 13-OCT-1999 (first entry)

DE Mouse Receptor 4-1BB protein.

XX Mouse Receptor 4-1BB CDNA; Mouse Receptor 4-1BB protein; H4-1BB protein;  
KW human 4-1BB protein; T cell activation; proliferation; immune response;  
KW receptor protein; autoimmune disease; organ transplantation;  
KW cancerous tumour; nerve growth factor receptor.  
XX

OS Mus musculus.

XX WO9936093-A1.

PN 22-JUL-1999.

XX 14-JAN-1999; 99WO-US000823.

XX 14-JAN-1998; 98US-00007097.

XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
(KWON/) KWON B S.

PI Kwon BS;

XX WPI; 1999-444325/37.

DR N-PSDB; AAX90763.

XX Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes

PT Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.

XX Disclosure; Page 75; 86pp; English.

XX The present sequence is mouse 4-1BB receptor protein. This protein has  
CC 65% homology with human receptor protein 4-1BB. The protein has a  
CC putative leader sequence, a potential membrane anchor segment and other  
CC features of known receptor proteins. 4-1BB is structurally related to  
CC members of the nerve growth factor receptor. Probes derived from mouse 4-  
CC 1BB CDNA are used to isolate cDNA of H4-1BB. The H4-1BB protein, its  
CC ligands, and various monoclonal antibodies have therapeutic uses. They  
CC may be used to enhance or suppress T cell activation and proliferation;  
CC for activation or inhibition of immune response; to block H4-1BB ligand  
CC binding; treating cancerous tumours and autoimmune diseases; and during  
CC organ transplantation  
XX

SQ Sequence 256 AA;

Query Match 100.0%; Score 62; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115

RESULT 8  
AAV33215

ID AAV33215 standard; protein; 256 AA.

XX  
AC AAV33215;

XX 18-NOV-1999 (first entry)

XX Murine CD137 protein.

XX CD137; monocyte growth factor; proliferation; peripheral monocyte;  
KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;  
KW immunostimulatory; non-specific immune response; phagocytosis;  
KW intracellular destruction; microorganism; immune complex; antibody;  
KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;  
KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;  
KW bacterial; viral infection; immunosuppressant; gene therapy; murine.  
XX

OS Mus sp.

XX WO9944629-A2.

XX 10-SEP-1999.

XX 05-MAR-1999; 99WO-EP001440.

XX 05-MAR-1998; 98EP-00103859.

XX (MERC ) MERCKLE GMBH.

XX Schwarz H, Langstein J;

XX WPI; 1999-550983/46.

XX Use of monocyte growth factor CD137 for stimulating proliferation of  
PT peripheral monocytes, particularly for treating immune deficiency, e.g.  
PT following cancer therapy.

XX Disclosure; Fig 1B; 57pp; German.

XX This invention describes a novel use of the human monocyte growth factor  
CC CD137, or its functional analogs, for (i) stimulating proliferation of  
CC peripheral monocytes; and (ii) treating diseases that are associated with  
CC disorders of a cellular system that includes monocytes (and/or their  
CC derived cells, precursor or progenitors) or where the origin and/or  
CC progression is treatable by stimulating proliferation of such cells. The  
CC products of the invention have antitumor, antibacterial, antiviral,  
CC antifungal and immunostimulatory activity. Stimulating proliferation of  
CC monocytes promotes the non-specific immune response, i.e. it increases  
CC phagocytosis and intracellular destruction of microorganisms, immune  
CC complexes and damaged cells, and improves antibody (in)dependent  
CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat  
CC diseases associated with a defective immune response where caused by  
CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation  
CC therapy; disorders of wound healing (e.g. in dialysis or diabetic  
CC patients; or those with chronic venous insufficiency); tumors; bacterial,  
CC fungal or viral infections; (non-)congenital or (non-)inherited diseases  
CC or injury to the immune system; injury induced by treatment with  
CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune  
CC disease, or transplant patients). Nucleic acid encoding (I) can be used  
CC similarly, in gene therapy procedures. Proliferation of peripheral  
CC monocytes is achieved independently of hematopoietic stem cells. This  
CC sequence represents the murine CD137 protein described in the method of

```
CC the invention
XX
SQ Sequence 256 AA;

Query Match      100.0%; Score 62; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
      |||||
Db      105 CRPGQELTKQG 115

RESULT 9
AAE22581
ID AAE22581 standard; protein; 256 AA.
XX
AC AAE22581;
XX
DT 26-JUL-2002 (first entry)
XX
DE Mouse receptore 4-1BB protein.
XX
KW Mouse; lymphokine; L2G25B; macrophage inflammatory protein 1 alpha;
KW MIP-1alpha; immune disease; myeloid progenitor cell differentiation;
KW 4-1BB; receptor.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT Protein /label= Signal_peptide
FT Modified-site 23..256
FT /note= "Mature receptor 4-1BB protein"
FT Modified-site 128..130
FT /note= "Asn is N-glycosylated"
FT Modified-site 138..140
FT /note= "Asn is N-glycosylated"
XX
PN US6355476-B1.
XX
PD 12-MAR-2002.
XX
PF 30-JUL-1992; 92US-00922996.
XX
PR 07-NOV-1988; 88US-00267577.
XX
PA (ADRE-) ADVANCED RES & TECHNOLOGY INC.
XX
PI Kwon BS, Broxmeyer HE;
XX
DR WPI; 2002-370577/40.
DR N-PSDB; AAD35694.
XX
PT New isolated and purified cDNA designated L25G25B encoding the mouse
PT lymphokine macrophage inflammatory protein 1 alpha which can be used for
PT modulating early myeloid progenitor cell differentiation.
XX
PS Disclosure; Fig 3; 81pp; English.
XX
CC The invention relates to an isolated and purified cDNA containing mouse
CC lymphokine designated L2G25B. L2G25B cDNA encodes lymphokine macrophage
CC inflammatory protein 1 alpha (MIP-1alpha). Lymphokines are proteins by
CC which the immune cells communicate with each other. Lymphokines are used
CC therapeutically against immunologic diseases. Mouse lymphokine MIP-alpha
CC can be used to modulate early myeloid progenitor cell differentiation.
CC The present sequence is mouse lymphokine receptor 4-1BB protein
XX
SQ Sequence 256 AA;

Query Match      100.0%; Score 62; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
      |||||
Db      105 CRPGQELTKQG 115

RESULT 11
ADC25939
ID ABB75954 standard; protein; 256 AA.
XX
AC ABB75954;
XX
DT 12-JUL-2002 (first entry)
XX
DE Murine cytokine receptor 4-1BB.
XX
KW Cytokine; receptor; 4-1BB; mouse.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT Protein /label= Signal_peptide
FT Modified-site 24..256
FT /label= Mature_protein
XX
PN US6355779-B1.
XX
PD 12-MAR-2002.
XX
PF 10-SEP-1998; 98US-00150864.
XX
PR 07-MAY-1993; 93US-00060843.
PR 06-MAY-1994; 94US-00236918.
PR 05-AUG-1997; 97US-00910449.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Goodwin RG, Smith CA, Alderson MR;
XX
DR WPI; 2002-380940/41.
DR N-PSDB; ABL54047.
XX
PT New antibody specific for the cytokine 4-1BB-ligand, useful for
PT immunoaffinity purification of the ligand.
XX
PS Example 1; Col 39-40; 31pp; English.
XX
CC The present sequence is the protein sequence of the murine cytokine
CC receptor, 4-1BB. A portion of the extracellular (ligand binding) domain
CC of the receptor was utilised in a murine 4-1BB/human IGG1 Fc fusion
CC protein, which was used to identify the murine 4-1BB ligand (4-1BB-L, see
CC ABB75952). The invention provides novel murine and human 4-1BB-L
CC polypeptides and human 4-1BB polypeptides, as well as DNA sequences
CC encoding them, recombinant expression vectors and host cells, and methods
CC for producing the novel polypeptides by cultivating the transformed host
CC cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from
CC their extracellular domains, have therapeutic value. Antibodies that are
CC immunoreactive with 4-1BB-L or human 4-1BB are claimed
XX
SQ Sequence 256 AA;

Query Match      100.0%; Score 62; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
      |||||
Db      105 CRPGQELTKQG 115

RESULT 11
ADC25939
```

ID XX ADC25939 standard; protein; 256 AA.  
 XX AC ADC25939;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE Murine receptor 4-1BB protein.  
 XX KW receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;  
 XX KW cancer; murine; mouse.  
 XX OS Mus musculus.  
 XX XX US2003100745-A1.  
 PN XX 29-MAY-2003.  
 PD XX  
 XX PF 04-FEB-2002; 2002US-00067122.  
 XX XX  
 XX PR 07-NOV-1988; 88US-00267577.  
 PR 30-JUL-1992; 92US-00922996.  
 PR 01-FEB-1993; 93US-00012269.  
 XX XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
 PA Kwon BS;  
 XX WPI; 2003-678138/64.  
 DR N-PSDB; ADC25938.  
 XX  
 PT New CDNA gene encoding receptor protein 4-1BB, useful for isolating  
 PT similar DNA sequences, and the encoded polypeptide and an antibody to it,  
 PT useful for identifying ligands, and for modulating immune cell activity.  
 XX  
 PS Claim 7; Fig 2; 77pp; English.  
 XX  
 CC The invention relates to a novel CDNA gene encoding receptor protein 4-  
 CC 1BB. The CDNA gene of the invention demonstrates immunostimulant  
 CC activities and may be useful as a probe to isolate DNA sequences encoding  
 CC for proteins similar to the receptor protein encoded by the DNA. The  
 CC protein, its fragments and derivatives may be useful as a probe to  
 CC isolate ligands to receptor protein 4-1BB, for stimulating proliferation  
 CC of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand  
 CC binding. The antibody may be useful for enhancing T-cell proliferation or  
 CC activation. Finally, the invention may be useful with respect to cancer  
 CC research. The current sequence is that of the murine receptor 4-1BB  
 CC protein of the invention.  
 XX SQ Sequence 256 AA;  
 Query Match 100.0%; Score 62; DB 7; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 0.0074;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CRPGQELTKQG 11  
 Db 105 CRPGQELTKQG 115  
 RESULT 12  
 ADE87549  
 ID ADE87549 standard; protein; 256 AA.  
 XX  
 AC ADE87549;  
 XX  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Mouse receptor H4-1BB.  
 XX KW immunosuppressive; H4-1BB ligand binding blocker; mouse;  
 KW receptor protein; H4-1BB; B-cell proliferation stimulator;  
 KW T-cell proliferation enhancer; immune system suppressor; transplantation;  
 KW autoimmune disease.

XX OS Mus sp.  
 XX PN US2003082157-A1.  
 XX PD 01-MAY-2003.  
 XX PF 12-JUN-2002; 2002US-00170997.  
 XX PR 07-NOV-1988; 88US-00267577.  
 PR 30-JUL-1992; 92US-00922996.  
 PR 01-FEB-1993; 93US-00012269.  
 PR 05-JUN-1995; 95US-00460976.  
 PR 22-OCT-1997; 97US-00955573.  
 XX (KWON/) KWON B S.  
 PA Kwon BS;  
 PI WPI; 2003-576599/54.  
 DR N-PSDB; ADE87548.  
 XX  
 PT New CDNA, or its encoded receptor protein H4-1BB, useful as probes to  
 PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking  
 PT H4-1BB ligand binding to facilitate organ transplantation or treat  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Fig 1; 19pp; English.  
 XX  
 CC The invention describes a CDNA, which encodes for human receptor protein  
 CC H4-1BB. The CDNA, or its fragments or derivatives, are useful as a probe  
 CC to isolate DNA sequences encoding for proteins similar to the receptor  
 CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or  
 CC derivatives, is useful as a probe for identifying ligands to the receptor  
 CC protein H4-1BB, or for stimulating the proliferation of B-cells  
 CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are  
 CC useful for enhancing T-cell proliferation of activation. The CDNA or  
 CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand  
 CC binding, which is particularly useful for suppressing the immune system  
 CC during transplantation, or for treating autoimmune diseases. This is the  
 CC amino acid sequence of mouse receptor H4-1BB.  
 XX SQ Sequence 256 AA;  
 Query Match 100.0%; Score 62; DB 7; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 0.0074;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CRPGQELTKQG 11  
 Db 105 CRPGQELTKQG 115  
 RESULT 13  
 AAE22582  
 ID AAE22582 standard; peptide; 12 AA.  
 XX AC AAE22582;  
 XX DT 26-JUL-2002 (first entry)  
 XX DE Mouse receptore 4-1BB peptide.  
 XX KW Mouse; lymphokine; L2G25B; macrophage inflammatory protein 1 alpha;  
 KW MIP-1alpha; immune disease; myeloid progenitor cell differentiation;  
 KW 4-1BB; receptor.  
 XX OS Mus sp.  
 XX PN US6355476-B1.  
 XX PD 12-MAR-2002.  
 XX

PF 30-JUL-1992; 92US-00922996.  
XX  
PR 07-NOV-1988; 88US-00267577.  
XX  
XX (ADRE-) ADVANCED RES & TECHNOLOGY INC.  
PA  
XX Kwon BS, Broxmeyer HE;  
PI  
XX WPI; 2002-370577/40.  
DR  
XX New isolated and purified cDNA designated L2G25B encoding the mouse  
XX lymphokine macrophage inflammatory protein 1 alpha which can be used for  
PT modulating early myeloid progenitor cell differentiation.  
PT  
XX Disclosure; Col 53; 81pp; English.  
PS  
XX The invention relates to an isolated and purified cDNA containing mouse  
CC lymphokine designated L2G25B. L2G25B cDNA encodes lymphokine macrophage  
CC inflammatory protein 1 alpha (MIP-1alpha). Lymphokines are proteins by  
CC which the immune cells communicate with each other. Lymphokines are used  
CC therapeutically against immunologic diseases. Mouse lymphokine MIP-alpha  
CC can be used to modulate early myeloid progenitor cell differentiation.  
CC The present sequence is mouse lymphokine receptor 4-1BB peptide  
XX  
XX Sequence 12 AA;  
SQ  
Query Match 91.9%; Score 57; DB 5; Length 12;  
Best Local Similarity 90.9%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 1 CRPGQELTKSG 11  
RESULT 14  
ADC25944  
ID ADC25944 standard; peptide; 12 AA.  
XX  
AC ADC25944;  
XX  
XX 18-DEC-2003 (first entry)  
XX Murine receptor 4-1BB peptide containing residues 105-115.  
DE  
XX receptor 4-1BB; immunostimulant; B-cell activation; T-cell proliferation;  
KW cancer; murine; mouse.  
KW  
XX Synthetic.  
OS Mus musculus.  
OS  
XX US2003100745-A1.  
XX  
XX 29-MAY-2003.  
PD  
XX 04-FEB-2002; 2002US-00067122.  
PF  
XX 07-NOV-1988; 88US-00267577.  
PR 30-JUL-1992; 92US-00922996.  
PR 01-FEB-1993; 93US-00012269.  
XX  
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
PA  
XX Kwon BS;  
PI  
XX WPI; 2003-678138/64.  
DR  
XX New cDNA gene encoding receptor protein 4-1BB, useful for isolating  
PT similar DNA sequences, and the encoded polypeptide and an antibody to it,  
PT useful for identifying ligands, and for modulating immune cell activity.  
XX  
XX Disclosure; Page 14; 77pp; English.  
PS  
XX

CC The invention relates to a novel cDNA gene encoding receptor protein 4-  
CC 1BB. The cDNA gene of the invention demonstrates immunostimulant  
CC activities and may be useful as a probe to isolate DNA sequences encoding  
CC for proteins similar to the receptor protein encoded by the DNA. The  
CC protein, its fragments and derivatives may be useful as a probe to  
CC isolate ligands to receptor protein 4-1BB, for stimulating proliferation  
CC of B cells expressing 4-1BB ligands and for blocking 4-1BB ligand  
CC binding. The antibody may be useful for enhancing T-cell proliferation or  
CC activation. Finally, the invention may be useful with respect to cancer  
CC research. The current sequence is that of the murine receptor 4-1BB  
CC peptide of the invention which contains residues 105-115.  
XX  
XX Sequence 12 AA;  
SQ  
Query Match 91.9%; Score 57; DB 7; Length 12;  
Best Local Similarity 90.9%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 1 CRPGQELTKSG 11  
RESULT 15  
AAR74087  
ID AAR74087 standard; protein; 255 AA.  
XX  
AC AAR74087;  
XX  
DT 21-JAN-1996 (first entry)  
XX  
DE Human receptor induced by lymphocyte activation (ILA).  
XX  
XX ILA; receptor inducible by lymphocyte activation; disease diagnosis;  
KW antiinflammatory.  
KW  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..17 /note= "signal peptide"  
FT Misc-difference 138 /note= "potential N-glycosylation site"  
FT Misc-difference 149 /note= "potential N-glycosylation site"  
FT Domain 187..213 /note= "transmembrane domain"  
FT Misc-difference 234 /note= "casein-kinase-II phosphorylation site"  
FT Misc-difference 235 /note= "casein-kinase-II phosphorylation site"  
FT Binding-site 241..244 /note= "potential ligand binding site"  
FT Misc-difference 242 /note= "protein-kinase phosphorylation site"  
XX  
XX CA2108401-A.  
PN  
XX 28-MAR-1995.  
PD  
XX 14-OCT-1993; 93CA-02108401.  
PF  
XX 27-SEP-1993; 93US-00127693.  
PR  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX Lotz M, Schwarz H;  
PI  
XX WPI; 1995-194420/26.  
DR N-PSDB; AAR74087.  
DR  
XX New receptor inducible by lymphocyte activation - used to develop prods.  
PT for the diagnosis and treatment of inflammatory host defence pathology.  
XX

XX PS Claim 55; Page 61; 91pp; English.

XX CC ILA may be used to identify a host defence inflammatory response in body

CC CC tissue. The ILA agents can be used to detect an ILA-mediated pathology

CC CC such as atherosclerosis, autoimmune disease (rheumatoid arthritis,

CC CC transplant rejection, pathogenic host defense responses to microorganism

CC CC and malignancy such as lung carcinoma

XX SQ Sequence 255 AA;

Query Match 80.6%; Score 50; DB 2; Length 255;

Best Local Similarity 81.8%; Pred. No. 1.1;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 106 CRQGQELTKKG 116

RESULT 16

AAAY94714

ID AAY94714 standard; protein; 132 AA.

XX AC AAY94714;

XX DT 29-JAN-2001 (first entry)

XX DE Tumour necrosis factor receptor (TNFR) domain of 4-1BB protein.

XX KW Tumour necrosis factor-receptor related protein; TR2; human; cancer;

KW Chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;

KW immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;

KW severely combined immunodeficiency; apoptosis inhibition;

KW Alzheimer's disease; Parkinson's disease; Crohn's disease.

XX OS Homo sapiens.

XX PN WO200056405-A2.

XX PD 28-SEP-2000.

XX PF 22-MAR-2000; 2000WO-US007521.

XX PR 22-MAR-1999; 99US-0125683P.

PR 26-MAR-1999; 99US-0126522P.

PR 20-MAY-1999; 99US-0135169P.

PR 06-AUG-1999; 99US-0147383P.

XX (NIJJ/) NI J.

PA (ROSE/) ROSEN C A.

PA (GENT/) GENTZ R L.

XX Ni J, Rosen CA, Gentz RL;

XX WPI; 2000-594519/56.

XX Nucleic acid molecule encoding a human tumor necrosis factor receptor 2

PT and its two splice variants, useful for treating arthritis or

PT inflammation, cancer (such as follicular lymphomas) and immunodeficiency

PT disorders.

XX Disclosure; Fig 16; 373pp; English.

XX CC This invention relates to an isolated nucleic acid molecule encoding a

CC human tumour necrosis factor (TNF)-receptor related protein TR2. Included

CC in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.

CC The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a

CC member of the TNFR superfamily. The invention includes a method for the

CC treatment of arthritis or inflammation using an antibody directed against

CC a fragment of the TR2 protein. TR2 its agonists, antagonists and

CC antibodies exhibit cytostatic, dermatological, antianaemic,

CC immunosuppressive, antiallergic, antiarthritic, antiasthmatic,

CC antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and

CC cerebroprotective activity. The methods are useful for treating arthritis

CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53

CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an

CC immunodeficiency or for enhancing an in vivo leukocyte response to an

CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or

CC preventing autoimmune diseases (such as autoimmune haemolytic anaemia,

CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and

CC inflammatory myopathies) and immunodeficiency disorders (such as severely

CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative

CC disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,

CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or

CC antagonists are useful for treating or preventing autoimmune diseases and

CC inhibit the growth, progression and/or metastasis of cancers. They are

CC also used to activate, differentiate or proliferate cancerous cells or

CC tissues, and can be used to treat diseases associated with increased cell

CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,

CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful

CC as sources for generating antibodies, as molecular weight markers. This

CC sequence represents the tumour necrosis factor receptor (TNFR) domain of

CC the human 4-1BB protein. The sequence was used in the characterisation of

CC the TR2 receptor protein of the invention

XX SQ Sequence 132 AA;

Query Match 75.8%; Score 47; DB 3; Length 132;

Best Local Similarity 72.7%; Pred. No. 1.9;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 79 CRQGQELTKKG 89

## RESULT 17

AAW31759

ID AAW31759 standard; protein; 219 AA.

XX AC AAW31759;

XX DT 01-APR-1998 (first entry)

XX DE A novel human h4-1BBSV receptor.

XX KW h4-1BBSV receptor; 4-1BB receptor splicing variant; endotoxin shock;

KW tumour necrosis factor; TNF ligand; T-cell activation; inflammation;

KW tumour prevention; viral infection; autoimmune disease;

XX cellular proliferation.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..18 /note= "putative signal sequence"

FT Protein 19..219 /note= "mature protein"

FT Domain 19..150

FT Domain /note= "soluble extracellular domain"

FT Domain 151..177 /note= "transmembrane domain"

XX PN WO9733898-A1.

XX PD 18-SEP-1997.

XX PF 15-MAR-1996; 96WO-US003587.

XX PR 15-MAR-1996; 96WO-US003587.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Yu G, Gentz RL;

XX



```

CC represented in Fig 2
XX Sequence 219 AA;
SQ
  Query Match      75.8%; Score 47; DB 2; Length 219;
  Best Local Similarity 72.7%; Pred. No. 3.2;
  Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11
Db 70 CKQGQELTKKG 80

RESULT 20
AAE08545
ID AAE08545 standard; protein; 219 AA.
XX
AC AAE08545;
XX
DT 15-NOV-2001 (first entry)
XX
DE Human h4-1BB splicing variant (h4-1BBSV) receptor.
XX
KW Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;
KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxigenic shock;
KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;
KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;
KW bone resorption; human immunodeficiency virus; HIV; graft rejection;
KW inflammation; antibacterial; immunosuppressive; vulnerable; vasotropic;
KW antiinflammatory; protozoicide; cachexia; immunomodulator; virucide.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .18
FT /label= Signal_peptide
FT Protein 19. .219
FT /label= Mature_human_h4-1BBSV_receptor
FT Domain 19. .150
FT /label= Extracellular_domain
FT Domain 151. .177
FT /label= Transmembrane_domain
XX
PN US2001014465-A1.
XX
PD 16-AUG-2001.
XX
PF 19-DEC-2000; 2000US-00739394.
XX
PR 15-MAR-1996; 96US-0013474P.
PR 13-MAR-1997; 97US-00816605.
PR 22-FEB-1999; 99US-00253549.
XX
PA (NIJJ/) NI J.
PA (YUGG/) YU G.
PA (GENT/) GENTZ R.
PA (DILL/) DILLON P J.
XX
PI Ni J, Yu G, Gentz R, Dillon PJ;
XX
DR WPI; 2001-529104/58.
DR N-PSDB; AAD15246.
XX
PT New human 4-1BB receptor splicing variant polypeptides and
PT polynucleotides, useful for research, diagnosis, prevention and treatment
PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency
PT syndrome and graft rejection.
XX
PS Claim 15; Fig 1; 28pp; English.
XX
CC The present invention relates to an isolated human 4-1BB receptor
CC splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis
CC factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in

```

Gene therapy. h4-1BBSV is useful for research, biological, clinical and therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives are useful as an immunogen to produce antibodies which are useful for isolating and identifying clones expressing the polypeptide or to purify the polypeptide. h4-1BBSV is useful for diagnosis and treatment of disorders of cells, tissues and organisms and its nucleic acid is useful for detecting complementary polynucleotides for e.g. as a diagnostic reagent and for chromosomal identification. h4-1BBSV receptor agonists are useful for preventing, treating tumours, restenosis, cytotoxicity, bacterial and viral infection, deleterious effects of ionising radiation, autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-host rejection, to regulate immune responses, wound healing and cellular proliferation and antagonists are useful for treating and/or preventing endotoxigenic shock, inflammation, cerebral malaria, activation of human immunodeficiency virus (HIV) virus, bone resorption, graft rejection and cachexia. The present sequence is human h4-1BBSV receptor

Sequence 219 AA;

Query Match 75.8%; Score 47; DB 4; Length 219;  
Best Local Similarity 72.7%; Pred. No. 3.2;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
Db 70 CKQGQELTKKG 80

RESULT 21  
ABB84639  
ID ABB84639 standard; protein; 219 AA.  
XX  
AC ABB84639;  
XX  
DT 05-FEB-2003 (first entry)  
XX  
DE Human h4-1BBSV receptor.  
XX  
KW Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive;  
KW anti-HIV; antibacterial; antiinflammatory; protozoicide; immunomodulator;  
KW vasotropic; gene therapy; chromosome mapping; extracellular domain;  
KW endotoxigenic shock; cytotoxicity; cerebral malaria; autoimmune disease;  
KW human immunodeficiency virus; HIV; graft-host rejection; bone resorption;  
KW cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;  
KW AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis;  
KW autoimmune disease.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .18  
FT /label= leader\_sequence  
FT Protein 19. .219  
FT /label= h4-1BBSV\_receptor  
FT /note= "region specifically claimed in claim 1b"  
FT Domain 19. .150  
FT /label= soluble\_extracellular\_domain  
FT /note= "region specifically claimed in claim 1a"  
FT Domain 151. .177  
FT /label= transmembrane\_domain  
XX  
PN US2002127651-A1.  
XX  
PD 12-SEP-2002.  
XX  
PF 15-MAR-2002; 2002US-00097330.  
XX  
PR 15-MAR-1996; 96US-0013474P.  
PR 13-MAR-1997; 97US-00816605.  
PR 22-FEB-1999; 99US-00253549.  
PR 19-DEC-2000; 2000US-00739394.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Gentz RL, Dillon PJ;  
PI WPI; 2003-066900/06.  
XX N-PSDB; ABS57520.  
DR  
XX Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors,  
PT providing resistance to bacteria, viruses and parasites, to induce  
PT proliferation of endothelial cells, and to treat restenosis.  
XX Example 2; Fig 1A-B; 29pp; English.  
PS  
XX This invention describes a novel human h4-1BBSV receptor or a sequence  
CC that is at least 85% identical to the h4-1BBSV receptor. The product of  
CC the invention has anti-tumour, virucide, immunosuppressive, anti-HIV,  
CC antibacterial, antiinflammatory, protozoacide, immunomodulator and  
CC vasotropic activity and can be used for gene therapy and chromosome  
CC mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to  
CC a disease related to underexpression of h4-1BBSV or for identifying  
CC agonists and antagonists. The soluble extracellular domain of h4-1BBSV  
CC receptor polypeptide is useful for treating and/or preventing endotoxic  
CC shock, cytotoxicity, inflammation, cerebral malaria, activation of human  
CC immunodeficiency virus (HIV), graft-host rejection, bone resorption or  
CC cachexia, tumours, autoimmune disease, ionizing radiation, acquired  
CC immunodeficiency syndrome (AIDS), for providing resistance to bacteria,  
CC viruses and parasites, to induce proliferation of endothelial cells and  
CC certain haematopoietic cells, to treat restenosis and to prevent certain  
CC autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.  
CC This sequence represents the human 4-1BBSV receptor described in the  
CC disclosure of the invention  
XX  
SQ Sequence 219 AA;

Query Match 75.8%; Score 47; DB 6; Length 219;  
Best Local Similarity 72.7%; Pred. No. 3.2;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELTKQG 11  
|: |||||:  
Db 70 CKQGQELTKKG 80

RESULT 22  
AAR64197  
ID AAR64197 standard; protein; 255 AA.  
XX  
AC AAR64197;  
XX  
DT 25-MAR-2003 (revised)  
DT 08-AUG-1995 (first entry)  
XX  
DE Human 4-1BB polypeptide.  
XX  
KW T-cell; lymphocyte; activation; tissue culture; clone; cell lines;  
KW proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.  
XX  
OS Homo sapiens.  
XX WO9426290-A1.  
XX  
PD 24-NOV-1994.  
XX  
PF 06-MAY-1994; 94WO-US005036.  
XX  
PR 07-MAY-1993; 93US-00060843.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Goodwin RG, Smith CA, Alderson MR;  
XX  
DR WPI; 1995-022265/03.  
DR N-PSDB; AAQ75424.  
XX

PT Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor 4-1BB  
PT to transduce signal.  
XX  
PS Claim 39; Page 47-48; 65pp; English.  
XX  
CC The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see AAQ75423)  
CC are useful in a pharmaceutical composition for stimulating the immune  
CC system. The 4-1BB and 4-1BB-L polypeptides are also useful for exploring  
CC mechanisms of T-cell activation, as they are expressed on T lymphocytes.  
CC 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation  
CC of primary T-cells during the derivation of clonal T-cell lines. It may  
CC also be used to stimulate proliferation of activated T-cells, used in  
CC therapeutic procedures. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 2; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELTKQG 11  
|: |||||:  
Db 106 CKQGQELTKKG 116

RESULT 23  
AAR70977  
ID AAR70977 standard; protein; 255 AA.  
XX  
AC AAR70977;  
XX  
DT 25-MAR-2003 (revised)  
DT 16-OCT-1995 (first entry)  
XX  
DE H4-1BB receptor protein.  
XX  
KW H4-1BB; receptor protein; immunosuppressive; autoimmune disease;  
KW organ transplantation; cell membrane ligand.  
XX  
OS Homo sapiens.  
XX WO9507984-A1.  
XX  
PD 23-MAR-1995.  
XX  
PF 15-SEP-1994; 94WO-US010457.  
XX  
PR 16-SEP-1993; 93US-00122796.  
XX  
PA (INDV ) UNIV INDIANA FOUND.  
XX  
PI Kwon BS;  
XX  
DR WPI; 1995-131352/17.  
DR N-PSDB; AAQ86126.  
XX  
PT Novel cDNA encoding human receptor protein H4-1BB - useful to produce the  
PT protein which is used to treat auto:immune disease and facilitate organ  
PT transplantation.  
XX  
PS Claim 6; Fig 2; 36pp; English.  
XX  
CC Human peripheral blood lymphocyte-derived cDNA was amplified by PCR using  
CC probes based on the mouse receptor protein 4-1BB gene. The PCR product  
CC was used to screen a cDNA library of activated human T-cells. The  
CC isolated cDNA (AAQ86126), deposited as NRRL AAB21131, encoded the human  
CC homolog, H4-1BB (AAR70977), of 4-1BB. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 2; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

RESULT 24  
AAW04174  
ID AAW04174 standard; protein; 255 AA.  
XX  
AC AAW04174;  
XX  
DT 12-DEC-1996 (first entry)  
XX  
DE Human receptor H4-1BB.  
XX  
KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;  
KW B-lymphocyte; B-cell; immunostimulant; cancer; autoimmune disease;  
KW graft rejection; therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO9629348-A1.  
XX  
PD 26-SEP-1996.  
XX  
PF 22-MAR-1996; 96WO-US003965.  
XX  
PR 23-MAR-1995; 95US-00409851.  
XX  
PA (INDV ) UNIV INDIANA FOUND.  
XX  
PI Kwon BS, Kang C;  
XX  
DR WPI; 1996-443138/44.  
DR N-PSDB; AAT39546.  
XX  
PT Monoclonal antibody specific for human receptor protein 4-1BB - used to  
PT enhance proliferation and activation of T-cells for treatment of cancer  
PT and to inhibit specific ligand binding for treating autoimmune diseases.  
XX  
PS Disclosure; Page 36-37; 48pp; English.  
XX  
CC Novel human receptor protein H4-1BB (AAW04174) has the potential to  
CC function as an accessory signaling molecule during T-cell activation and  
CC proliferation. Its amino acid sequence was deduced from a cDNA clone  
CC (AAT39546) isolated from activated human T-lymphocytes. Recombinant H4-  
CC 1BB can be produced in transfected host cells. It is used to isolate  
CC receptor ligands, to stimulate B-cells expressing such ligands and to  
CC block H4-1BB ligand binding. A fusion protein of H4-1BB with human  
CC placental alkaline phosphatase can be used to modify immune responses. A  
CC monoclonal antibody raised against an immunopeptide (see also AAW04172)  
CC of H4-1BB is useful in the treatment of cancer and autoimmune diseases  
XX  
SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 2; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

RESULT 25  
AAW26658  
ID AAW26658 standard; protein; 255 AA.  
XX  
AC AAW26658;  
XX  
DT 25-MAR-2003 (revised)

DT 25-FEB-1998 (first entry)  
XX  
DE Human 4-1BB receptor.  
XX  
KW 4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte; T cell;  
KW proliferation; immunostimulant.  
XX  
OS Homo sapiens.  
XX  
PN Location/Qualifiers  
FT Key 1..23  
FT Peptide /label= sig\_peptide  
FT Domain 24..186  
FT /label= Cytoplasmic  
FT Modified-site 115..117  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 126..128  
FT /note= "Asn is N-glycosylated"  
FT Domain 187..213  
FT /label= Transmembrane  
FT Domain 214..255  
FT /label= Extracellular  
XX  
PN US5674704-A.  
XX  
PD 07-OCT-1997.  
XX  
PF 06-MAY-1994; 94US-00236918.  
XX  
PR 07-MAY-1993; 93US-00060843.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Alderson MR, Goodwin RG, Smith CA;  
XX  
DR WPI; 1997-502333/46.  
DR N-PSDB; AAT91026.  
XX  
PT DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell  
PT proliferation in vitro, and as research tools.  
XX  
PS Example 2; Col 43-44; 32pp; English.  
XX  
CC This protein comprises human 4-1BB, a member of the tumour necrosis  
CC factor receptor superfamily that is expressed on cells that include, but  
CC are not limited to, stimulated human peripheral blood lymphocytes. Its  
CC amino acid sequence was deduced from an isolated cDNA clone (see  
CC AAT91026) obtained from human peripheral blood T-lymphocytes. A novel  
CC claimed cytokine, designated 4-1BB ligand (4-1BB-L) has been identified,  
CC cloned and sequenced (see AAW26657) that binds to 4-1BB. 4-1BB-L,  
CC especially its soluble extracellular domain, can be used to stimulate T-  
CC cell proliferation in vitro, as a research tool and as an affinity ligand  
CC for purifying 4-1BB. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 2; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

RESULT 26  
AAW28688  
ID AAW28688 standard; protein; 255 AA.  
XX  
AC AAW28688;  
XX  
DT 13-OCT-1999 (first entry)  
XX

DE Human receptor protein 4-1BB.  
XX  
KW Human receptor protein 4-1BB; H4-1BB; T cell activation; proliferation;  
KW mouse 4-1BB cDNA; monoclonal antibody; immune response;  
KW organ transplantation; autoimmune disease; diabetes; cancerous tumour;  
KW rheumatoid arthritis; lupus; nerve growth factor receptor.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Protein 18..255  
FT /note= "Purified human 4-1BB"  
XX  
PN WO9936093-A1.  
XX  
PD 22-JUL-1999.  
XX  
PF 14-JAN-1999; 99WO-US0000823.  
XX  
PR 14-JAN-1998; 98US-00007097.  
XX  
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
PA (KWON/) KWON B S.  
XX  
PI Kwon BS;  
XX  
DR WPI; 1999-444325/37.  
DR N-PSDB; AAZ08961.  
XX  
PT Using human receptor protein 4-1BB ligands to, e.g. treat Diabetes  
PT Mellitus, Rheumatoid Arthritis and Systemic Lupus Erythematosus.  
XX  
PS Claim 4; Page 77-78; 86pp; English.  
XX  
CC The present sequence is a human receptor protein 4-1BB. 4-1BB is  
CC structurally related to members of the nerve growth factor receptor. It  
CC contains a putative zinc finger structure similar to that of yeast eIF-2b  
CC protein. Probes derived from mouse 4-1BB cDNA are used to isolate cDNA of  
CC H4-1BB. The H4-1BB protein, its ligands, and various monoclonal  
CC antibodies have therapeutic uses. They may be used to enhance or suppress  
CC T cell activation and proliferation; B cell proliferation; treating  
CC cancerous tumours and AIDS. The use of H4-1BB to block H4-1BB ligand  
CC binding has practical application in the suppression of immune system  
CC during organ transplantation or against autoimmune diseases including  
CC diabetes, rheumatoid arthritis, and lupus  
XX  
SQ Sequence 255 AA;  
Query Match 75.8%; Score 47; DB 2; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 106 CKQGQELTKKG 116  
RESULT 27  
AAAY33214  
ID AAY33214 standard; protein; 255 AA.  
XX  
AC AAY33214;  
XX  
DT 18-NOV-1999 (first entry)  
XX  
DE Human CD137 protein.  
XX  
KW CD137; monocyte growth factor; proliferation; peripheral monocyte;  
KW treatment; disease; antitumor; antibacterial; antiviral; antifungal;  
KW immunostimulatory; non-specific immune response; phagocytosis;  
KW intracellular destruction; microorganism; immune complex; antibody;  
KW cytotoxicity; tumor cell; macrophage; hematopoietic system; leucopenia;  
KW chemotherapy; radiation; therapy; wound healing disorder; tumor; fungal;

KW bacterial; viral infection; immunosuppressant; gene therapy; human.  
XX  
OS Homo sapiens.  
XX  
PN WO9944629-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 05-MAR-1999; 99WO-EP001440.  
XX  
PR 05-MAR-1998; 98EP-00103859.  
XX  
PA (MERC ) MERCKLE GMBH.  
XX  
PI Schwarz H, Langstein J;  
XX  
DR WPI; 1999-550983/46.  
DR N-PSDB; AAZ09769.  
XX  
PT Use of monocyte growth factor CD137 for stimulating proliferation of  
PT peripheral monocytes, particularly for treating immune deficiency, e.g.  
PT following cancer therapy.  
XX  
PS Claim 12; Fig 1A; 57pp; German.  
XX  
CC This invention describes a novel use of the human monocyte growth factor  
CC CD137, or its functional analogs, for (i) stimulating proliferation of  
CC peripheral monocytes; and (ii) treating diseases that are associated with  
CC disorders of a cellular system that includes monocytes (and/or their  
CC derived cells, precursor or progenitors) or where the origin and/or  
CC progression is treatable by stimulating proliferation of such cells. The  
CC products of the invention have antitumor, antibacterial, antiviral,  
CC antifungal and immunostimulatory activity. Stimulating proliferation of  
CC monocytes promotes the non-specific immune response, i.e. it increases  
CC phagocytosis and intracellular destruction of microorganisms, immune  
CC complexes and damaged cells, and improves antibody (in)dependent  
CC cytotoxicity to tumor cells. CD137 is used, in vivo or ex vivo, to treat  
CC diseases associated with a defective immune response where caused by  
CC inadequate numbers of active monocytes/macrophages, especially damage to  
CC the hematopoietic system (leucopenia) caused by chemotherapy or radiation  
CC therapy; disorders of wound healing (e.g. in dialysis or diabetic  
CC patients, or those with chronic venous insufficiency); tumors; bacterial,  
CC fungal or viral infections; (non-)congenital or (non-)inherited diseases  
CC or injury to the immune system; injury induced by treatment with  
CC immunosuppressants (e.g. patients with chronic arthritis or autoimmune  
CC disease, or transplant patients). Nucleic acid encoding (I) can be used  
CC similarly, in gene therapy procedures. Proliferation of peripheral  
CC monocytes is achieved independently of hematopoietic stem cells. This  
CC sequence represents the human CD137 protein described in the method of  
CC the invention  
XX  
SQ Sequence 255 AA;  
Query Match 75.8%; Score 47; DB 2; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 106 CKQGQELTKKG 116  
RESULT 28  
AAE08546  
ID AAE08546 standard; protein; 255 AA.  
XX  
AC AAE08546;  
XX  
DT 15-NOV-2001 (first entry)  
XX  
DE Human h4-1BB receptor.  
XX  
KW Human; h4-1BB receptor splicing variant; h4-1BBSV; gene therapy; tumour;

KW tumour necrosis factor; TNF; restenosis; cytotoxicity; endotoxin shock;  
 KW wound healing; autoimmune disease; acquired immunodeficiency syndrome;  
 KW AIDS; graft-host rejection; cellular proliferation; cerebral malaria;  
 KW bone resorption; human immunodeficiency virus; HIV; graft rejection;  
 KW inflammation; antibacterial; immunosuppressive; vulnary; vasotropic;  
 KW antiinflammatory; protozoicide; cachexia; immunomodulator; virucide.

OS Homo sapiens.

XX US2001014465-A1.

XX 16-AUG-2001.

XX 19-DEC-2000; 2000US-00739394.

XX 15-MAR-1996; 96US-0013474P.

XX 13-MAR-1997; 97US-00816605.

XX 22-FEB-1999; 99US-00253549.

XX (NIJ/J) NI J.

XX (YUGG/) YU G.

XX (GENT/) GENTZ R.

XX (DILL/) DILLON P J.

XX NI J, Yu G, Gentz R, Dillon PJ;

XX WPI; 2001-529104/58.

XX New human 4-1BB receptor splicing variant polypeptides and

PT polynucleotides, useful for research, diagnosis, prevention and treatment  
 PT of tumors, cytotoxicity, autoimmune diseases, acquired immunodeficiency  
 PT syndrome and graft rejection.

XX Disclosure; Fig 2; 28pp; English.

XX The present invention relates to an isolated human 4-1BB receptor  
 CC splicing variant (h4-1BBSV, where 4-1BB is a member of tumour necrosis  
 CC factor (TNF) family of ligands) polypeptide. h4-1BBSV cDNA is used in  
 CC gene therapy. h4-1BBSV is useful for research, biological, clinical and  
 CC therapeutic purposes. h4-1BBSV, its fragments, analogues or derivatives  
 CC are useful as an immunogen to produce antibodies which are useful for  
 CC isolating and identifying clones expressing the polypeptide or to purify  
 CC the polypeptide. h4-1BBSV is useful for diagnosis and treatment of  
 CC disorders of cells, tissues and organisms and its nucleic acid is useful  
 CC for detecting complementary polynucleotides for e.g. as a diagnostic  
 CC reagent and for chromosomal identification. h4-1BBSV receptor agonists  
 CC are useful for preventing, treating tumours, restenosis, cytotoxicity,  
 CC bacterial and viral infection, deleterious effects of ionising radiation,  
 CC autoimmune diseases, acquired immunodeficiency syndrome (AIDS) and graft-  
 CC host rejection, to regulate immune responses, wound healing and cellular  
 CC proliferation and antagonists are useful for treating and/or preventing  
 CC endotoxin shock, inflammation, cerebral malaria, activation of human  
 CC immunodeficiency virus (HIV) virus, bone resorption, graft rejection and  
 CC cachexia. The present sequence is human h4-1BB receptor

XX Sequence 255 AA;

Query Match 75.8%; Score 47; DB 4; Length 255;

Best Local Similarity 72.7%; Pred. No. 3.7;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 106 CKQGQELTKKG 116

RESULT 29

AAB50521

ID AAB50521 standard; protein; 255 AA.

XX AC

XX AAB50521;

XX 15-MAR-2001 (first entry)

XX

DE

XX

KW

KW

KW

KW

KW

KW

KW

KW

KW

XX

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

PA

XX

PI

XX

DR

XX

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Human tumour necrosis factor receptor 4-1BB protein SEQ ID NO:11.

Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;  
 TRAIL receptor without intracellular domain; diagnosis; cytostatic;  
 tumour necrosis factor related apoptosis inducing ligand; vasotropic;  
 immunosuppressive; neuroprotective; antiviral; antiinflammatory;  
 anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
 gene therapy; restenosis; graft versus host disease; tumour; cancer;  
 apoptotic cell death related disease; autoimmune disorder;  
 cardiovascular disorder; viral infection.

OS Homo sapiens.

XX WO2000071150-A1.

XX 30-NOV-2000.

XX 18-MAY-2000; 2000WO-US013515.

XX 20-MAY-1999; 99US-0135164P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Wei Y, Ruben SM, Gentz RL, Ni J;

XX WPI; 2001-041051/05.

XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
 PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
 PT prevention of cancer, autoimmune disorders and viral infection.

XX Disclosure; Fig 2; 285pp; English.

XX The present invention describes the human TRID protein (tumour necrosis  
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
 CC intracellular domain, also referred to as tumour necrosis factor receptor  
 CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nootropic,  
 CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic  
 CC activities, and can be used in gene therapy. The TRID polynucleotides are  
 CC useful for detecting complementary polynucleotides. TRID proteins and  
 CC polynucleotides are useful in the treatment of tumours, resistance to  
 CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
 CC They are also useful for inducing proliferation of T-cells, endothelial  
 CC cells and certain haematopoietic cells, to regulate antiviral responses  
 CC and to prevent certain autoimmune diseases after stimulation of TRID by  
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
 CC polypeptides are useful for treating and/or preventing diseases  
 CC associated with increased or decreased apoptotic cell death. The TRID  
 CC polynucleotides, proteins, antibodies, agonists and antagonists are  
 CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)  
 CC autoimmune disorders; (c) diseases associated with increased apoptosis;  
 CC (d) cardiovascular disorders; and (e) viral infection. The present  
 CC sequence represents a tumour necrosis factor receptor used in comparison  
 CC with TRID in the exemplification of the present invention

XX Sequence 255 AA;

Query Match 75.8%; Score 47; DB 4; Length 255;

Best Local Similarity 72.7%; Pred. No. 3.7;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 106 CKQGQELTKKG 116

RESULT 30

AB75955

ID AB75955 standard; protein; 255 AA.

XX AC

XX AB75955;

XX DT 12-JUL-2002 (first entry)  
XX DE Human cytokine receptor 4-1BB.  
XX KW Cytokine; receptor; 4-1BB; human.  
XX OS Homo sapiens.  
XX FH Location/Qualifiers  
FT Key  
FT Peptide 1. .23  
FT Protein /label= Signal\_peptide  
FT /label= Mature\_protein  
FT Domain 24. .186  
FT /note= "extracellular domain"  
FT Modified-site 138. .140  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 149. .151  
FT /note= "Asn is N-glycosylated"  
FT Region 186. .213  
FT /note= "transmembrane region"  
FT Domain 214. .255  
FT /note= "cytoplasmic domain"  
XX US6355779-B1.  
XX 12-MAR-2002.  
XX 10-SEP-1998; 98US-00150864.  
XX 07-MAY-1993; 93US-00060843.  
XX 06-MAY-1994; 94US-00236918.  
XX 05-AUG-1997; 97US-00910449.  
XX (IMV ) IMMUNEX CORP.  
XX Goodwin RG, Smith CA, Alderson MR;  
XX WPI; 2002-380940/41.  
XX N-PSDB; ABL54048.  
XX New antibody specific for the cytokine 4-1BB-ligand, useful for  
XX immunoaffinity purification of the ligand.  
XX Example 2; Col 43-44; 3lpp; English.  
XX The present sequence is the protein sequence of the human cytokine  
XX receptor, 4-1BB. The sequence was deduced from a cDNA clone (see  
XX ABL54048) obtained from a human peripheral blood T-lymphocyte cDNA  
XX library. It shows 60% identity to murine 4-1BB (see ABB75954). A portion  
XX of the extracellular (ligand binding) domain of the human 4-1BB cytokine  
XX receptor was utilised in a human 4-1BB/human IgG1 Fc fusion protein,  
XX which was used to identify the human 4-1BB ligand (4-1BB-L, see  
XX ABB75953). The invention provides novel murine and human 4-1BB-L  
XX polypeptides and human 4-1BB polypeptides, as well as DNA sequences  
XX encoding them, recombinant expression vectors and host cells, and methods  
XX for producing the novel polypeptides by cultivating the transformed host  
XX cells. Soluble forms of the 4-1BB-L and 4-1BB polypeptides, derived from  
XX their extracellular domains, have therapeutic value. Antibodies that are  
XX immunoreactive with 4-1BB-L or human 4-1BB are claimed  
XX  
XX Sequence 255 AA;  
XX  
XX Query Match 75.8%; Score 47; DB 5; Length 255;  
XX Best Local Similarity 72.7%; Pred. No. 3.7;  
XX Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 1 CRPGQELTKQG 11  
XX | : ||||| : |  
XX 106 CKQGQELTKG 116

RESULT 31  
ABR39863  
ID ABR39863 standard; protein; 255 AA.  
XX  
AC ABR39863;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Human MOCEPTIN polypeptide.  
XX  
KW MOCEPTIN; tumour necrosis factor receptor; TNF receptor; anorectic;  
KW antilipemic; antiarteriosclerotic; antidiabetic; cerebroprotective;  
KW hypotensive; immunomodulator; antidepressant; human; receptor.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1. .17  
XX /note= "putative signal peptide"  
XX Protein 18. .255  
XX /note= "mature protein"  
XX Domain 18. .186  
XX /note= "extracellular domain"  
XX Domain 187. .213  
XX /note= "transmembrane domain"  
XX Domain 214. .255  
XX /note= "intracellular domain"  
XX  
XX WO2003011325-A1.  
XX  
XX 13-FEB-2003.  
XX  
XX 25-JUL-2002; 2002WO-IB003499.  
XX  
XX 27-JUL-2001; 2001US-0308142P.  
XX  
XX (GEST ) GENSET SA.  
XX  
XX Lucas J, Dialynas D, Briggs K;  
XX  
XX WPI; 2003-268084/26.  
XX N-PSDB; ACC47324.  
XX  
XX New agonist and antagonist of MOCEPTIN (a member of the Tumor Necrosis  
XX Factor Receptor family) activity, useful for preventing or treating  
XX obesity-related diseases (e.g. hyperlipidemia or stroke), or increasing  
XX body mass.  
XX  
XX Disclosure; Page 32-33; 37pp; English.  
XX  
XX The invention relates to an agonist or antagonist of MOCEPTIN (a member  
XX of the Tumour Necrosis Factor Receptor family) activity. The antagonist  
XX or agonist of MOCEPTIN activity, or the composition comprising the  
XX agonist or antagonist, is useful for preventing or treating an obesity-  
XX related disorder or disease in an individual. In particular, the agonist  
XX of MOCEPTIN activity is useful for treating or preventing obesity-related  
XX diseases, e.g. hyperlipidemia, atherosclerosis, insulin resistance,  
XX diabetes, stroke or hypertension. The agonist is also useful for reducing  
XX body mass and maintaining weight loss. The antagonist of MOCEPTIN  
XX activity is useful for increasing body mass, or for treating or  
XX preventing disorders associated with excessive weight loss, e.g.  
XX cachexia, cancer-related weight loss, AIDS-related weight loss, chronic  
XX inflammatory disease-related weight loss, or anorexia. The present  
XX sequence represents a human MOCEPTIN polypeptide  
XX  
XX Sequence 255 AA;  
XX  
XX Query Match 75.8%; Score 47; DB 6; Length 255;  
XX Best Local Similarity 72.7%; Pred. No. 3.7;  
XX Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 1 CRPGQELTKQG 11  
XX | : ||||| : |

Db 106 CKQGQELTKKG 116

RESULT 32  
ABB84640  
ID ABB84640 standard; protein; 255 AA.  
XX AC ABB84640;  
XX DT 05-FEB-2003 (first entry)  
XX DE Human h4-1BB receptor.  
XX KW Human; h4-1BBSV receptor; anti-tumour; virucide; immunosuppressive;  
KW anti-HIV; antibacterial; antiinflammatory; protozoacide; immunomodulator;  
KW vasotropic; gene therapy; chromosome mapping; extracellular domain;  
KW endotoxic shock; cytotoxicity; cerebral malaria; autoimmune disease;  
KW human immunodeficiency virus; HIV; graft-host rejection; bone resorption;  
KW cachexia; tumour; ionizing radiation; acquired immunodeficiency syndrome;  
KW AIDS; endothelial cell; proliferation; haematopoietic cell; restenosis;  
KW autoimmune disease; h4-1BB.  
XX OS Homo sapiens.  
XX PN US2002127651-A1.  
XX PD 12-SEP-2002.  
XX PF 15-MAR-2002; 2002US-00097330.  
XX PR 15-MAR-1996; 96US-0013474P.  
XX PR 13-MAR-1997; 97US-00816605.  
XX PR 22-FEB-1999; 99US-00253549.  
XX PR 19-DEC-2000; 2000US-00739394.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Ni J, Yu G, Gentz RL, Dillon PJ;  
XX WPI; 2003-066900/06.  
XX PT Novel isolated h4-1BBSV receptor polypeptide, useful for treating tumors,  
PT providing resistance to bacteria, viruses and parasites, to induce  
PT proliferation of endothelial cells, and to treat restenosis.  
XX PS Disclosure; Fig 2; 29pp; English.  
XX CC This invention describes a novel human h4-1BBSV receptor or a sequence  
CC that is at least 85% identical to the h4-1BBSV receptor. The product of  
CC the invention has anti-tumour, virucide, immunosuppressive, anti-HIV,  
CC antibacterial, antiinflammatory, protozoacide, immunomodulator and  
CC vasotropic activity and can be used for gene therapy and chromosome  
CC mapping. h4-1BBSV is useful for diagnosing a disease or susceptibility to  
CC a disease related to underexpression of h4-1BBSV or for identifying  
CC agonists and antagonists. The soluble extracellular domain of h4-1BBSV  
CC receptor polypeptide is useful for treating and/or preventing endotoxic  
CC shock, cytotoxicity, inflammation, cerebral malaria, activation of human  
CC immunodeficiency virus (HIV), graft-host rejection, bone resorption or  
CC cachexia, tumours, autoimmune disease, ionizing radiation, acquired  
CC immunodeficiency syndrome (AIDS), for providing resistance to bacteria,  
CC viruses and parasites, to induce proliferation of endothelial cells and  
CC certain haematopoietic cells, to treat restenosis and to prevent certain  
CC autoimmune diseases after stimulation of h4-1BBSV receptor by an agonist.  
CC This sequence represents the human h4-1BB receptor described in the  
XX disclosure of the invention  
SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 6; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 106 CKQGQELTKKG 116

RESULT 33  
AAE39531  
ID AAE39531 standard; protein; 255 AA.  
XX AC AAE39531;  
XX DT 18-DEC-2003 (first entry)  
XX DE Human protein SEQ ID NO: 2.  
XX KW Human; adhesive; packaging.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Misc-difference 107  
FT /note= "Encoded by AGA"  
XX PN US2003000851-A1.  
XX PD 02-JAN-2003.  
XX PF 08-JUN-2001; 2001US-00877336.  
XX PR 08-JUN-2001; 2001US-00877336.  
XX PA (WALS/) WALSH J C.  
XX PA (HAWK/) HAWKINS K E.  
XX PI Walsh JC, Hawkins KE;  
XX WPI; 2003-266968/26.  
XX DR N-PSDB; AAD59981.  
XX PT Paper board container manufacture for soap boxes, involves applying  
PT adhesive on blank while moving in one direction, which is folded, and  
PT then another quantity of adhesive is applied before moving blank to  
XX another direction.  
XX PS Disclosure; Page 12-13; 46pp; English.  
XX CC The invention relates to a method and apparatus for applying adhesive to  
CC packaging in a variety of configurations. The method involves applying  
CC adhesive on blank while moving in one direction, which is folded, and  
CC then another quantity of adhesive is applied before moving blank to  
CC another direction. The invention is useful for e.g. soap boxes, cereal  
CC boxes, bottle carriers, can boxes. The present sequence is human protein.  
CC Note: There is no specific information about the sequence in the  
XX specification  
SQ Sequence 255 AA;

Query Match 75.8%; Score 47; DB 7; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 106 CKQGQELTKKG 116

RESULT 34  
ADC78803  
ID ADC78803 standard; protein; 255 AA.  
XX AC ADC78803;  
XX DT 01-JAN-2004 (first entry)

DE Human PRO protein #16.  
XX human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;  
KW Crohn's disease.  
XX  
OS Homo sapiens.  
XX  
EN WO2003034984-A2.  
XX  
PD 01-MAY-2003.  
XX  
PF 15-OCT-2002; 2002WO-US033070.  
XX  
PR 19-OCT-2001; 2001US-0340083P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Goddard A, Gurney AL;  
XX  
DR WPI; 2003-481990/45.  
XX  
DR N-PSDB; ADC78802.  
XX  
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a  
PT medicament for diagnosing or treating cancer or inflammatory bowel  
PT disorder e.g., ulcerative colitis or Crohn's disease.  
XX  
PS Claim 12; SEQ ID NO 32; 327pp; English.  
XX  
CC The invention comprises the amino acid and coding sequences of human PRO  
CC proteins. The DNA and protein sequences of the invention are useful for  
CC the diagnosis and treatment of cancer and inflammatory bowel disease  
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid  
CC sequence represents a human PRO protein of the invention.  
XX  
SQ Sequence 255 AA;  
Query Match 75.8%; Score 47; DB 7; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 106 CKQGQELTKKG 116  
RESULT 35  
ADD25599  
ID ADD25599 standard; protein; 255 AA.  
XX  
AC ADD25599;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Binding domain-immunoglobulin fusion protein-associated protein #77.  
XX  
KW Binding domain; immunoglobulin; fusion protein; cytostatic;  
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
KW neuroprotective; hinge region; immunoglobulin heavy chain;  
KW CH2 constant region; CH3 constant region; IGG1;  
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
XX  
OS Unidentified.  
XX  
PN US2003118592-A1.  
XX  
PD 26-JUN-2003.  
XX  
PF 25-JUL-2002; 2002US-00207655.  
XX  
PR 17-JAN-2001; 2001US-0367358P.

PR 17-JAN-2002; 2002US-00053530.  
PR 03-JUN-2002; 2002US-0385691P.  
XX  
PA (GENE-) GENE-CRAFT INC.  
XX  
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
XX  
DR WPI; 2003-801317/75.  
XX  
PT New binding domain-immunoglobulin fusion protein, useful for treating a  
PT subject having or suspected of having a malignant condition or a B-cell  
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
XX  
PS Disclosure; SEQ ID NO 160; 157pp; English.  
XX  
CC The invention relates to a binding domain-immunoglobulin fusion protein  
CC comprising a binding domain polypeptide that is fused to an  
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
CC CH2 constant region polypeptide that is fused to the hinge region  
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
CC polypeptide that is fused to the CH2 constant region polypeptide. The  
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin  
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
CC region polypeptide, derived from (a) having 3 or more cysteine residues;  
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
CC immunoglobulin hinge region polypeptide contains no more than one  
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
CC capable of at least one immunological activity comprising antibody  
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
CC binding domain polypeptide is capable of specifically binding to an  
CC antigen. Also included are an isolated polynucleotide encoding the  
CC binding domain-immunoglobulin fusion protein, a recombinant expression  
CC construct comprising the polynucleotide (operably linked to a promoter),  
CC a host cell transformed or transfected with a recombinant expression  
CC construct, producing the binding domain-immunoglobulin fusion protein, a  
CC pharmaceutical composition comprising the binding domain-immunoglobulin  
CC fusion protein or polynucleotide and a carrier, and treating a subject  
CC having or suspected of having a malignant condition or a B-cell disorder.  
CC The binding domain-immunoglobulin fusion protein is useful for treating a  
CC subject having or suspected of having a malignant condition or a B-cell  
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
CC sclerosis or autoimmune disease. The present sequence is a binding domain  
CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
CC sequence data for this patent formed part of the printed specification  
CC and is also available in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequences.html?DocID=20030118592. The authors have not  
CC identified the sequences in the printed specification by their SEQ ID  
CC number therefore none of the sequences can be explicitly identified.  
XX  
SQ Sequence 255 AA;  
Query Match 75.8%; Score 47; DB 7; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 106 CKQGQELTKKG 116  
RESULT 36  
ADE87541  
ID ADE87541 standard; protein; 255 AA.  
XX  
AC ADE87541;  
XX

DT 29-JAN-2004 (first entry)  
XX Unknown human receptor H4-1BB.  
DE  
XX immunosuppressive; H4-1BB ligand binding blocker; human;  
KW receptor protein; H4-1BB; B-cell proliferation stimulator;  
KW T-cell proliferation enhancer; immune system suppressor; transplantation;  
KW autoimmune disease.  
XX  
OS Homo sapiens.  
XX  
XX US2003082157-A1.  
XX  
XX 01-MAY-2003.  
XX  
XX 12-JUN-2002; 2002US-00170997.  
XX  
XX 07-NOV-1988; 88US-00267577.  
XX 30-JUL-1992; 92US-00922996.  
XX 01-FEB-1993; 93US-00012269.  
XX 05-JUN-1995; 95US-00460976.  
XX 22-OCT-1997; 97US-00955573.  
XX  
XX (KWON/) KWON B S.  
XX  
XX Kwon BS;  
XX  
XX WPI; 2003-576599/54.  
XX N-PSDB; ADE87540.  
XX  
XX New CDNA, or its encoded receptor protein H4-1BB, useful as probes to  
PT isolate DNAs or ligands to the receptor protein H4-1BB, or for blocking  
PT H4-1BB ligand binding to facilitate organ transplantation or treat  
PT autoimmune diseases.  
XX  
XX Disclosure; SEQ ID NO 2; 19pp; English.  
XX  
XX The invention describes a cDNA, which encodes for human receptor protein  
CC H4-1BB. The cDNA, or its fragments or derivatives, are useful as a probe  
CC to isolate DNA sequences encoding for proteins similar to the receptor  
CC protein H4-1BB. The receptor protein H4-1BB, or its fragments or  
CC derivatives, is useful as a probe for identifying ligands to the receptor  
CC protein H4-1BB, or for stimulating the proliferation of B-cells  
CC expressing H4-1BB ligands. The monoclonal antibodies against H4-1BB are  
CC useful for enhancing T-cell proliferation of activation. The cDNA or  
CC receptor protein H4-1BB is also useful for blocking H4-1BB ligand  
CC binding, which is particularly useful for suppressing the immune system  
CC during transplantation, or for treating autoimmune diseases. This is the  
CC amino acid sequence of unknown human receptor H4-1BB.  
XX  
XX Sequence 255 AA;  
SQ  
Query Match 75.8%; Score 47; DB 7; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CRQGQELTKKG 116  
RESULT 37  
AAE29933  
ID AAE29933 standard; protein; 265 AA.  
XX  
XX AAE29933;  
XX  
XX 24-FEB-2003 (first entry)  
DT Human LP283 splice variant protein, LP346.  
DE  
XX Human; LP protein; cell proliferative disorder; actinic keratinosis;  
KW arteriosclerosis; psoriasis; leukaemia; lymphoma; autoimmune disorder;  
KW

KW melanoma; cancer; inflammatory disorder; Addison's disease; allergy;  
KW acquired immune deficiency syndrome; AIDS; ankylosing spondylitis;  
KW amyloidosis; anaemia; asthma; Crohn's disease; Goodpasture's syndrome;  
KW gout; Grave's disease; Hashimoto's thyroiditis; cardiovascular disorder;  
KW congestive heart failure; ischaemic heart disease; myocardial infarction;  
KW angina pectoris; atherosclerosis; hypertension; neurological disorder;  
KW stroke; Parkinson's disease; Alzheimer's disease; developmental disorder;  
KW Down's syndrome; cerebral palsy; gene therapy; nephrotropic; nontropic.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX WO200274906-A2.  
XX  
XX 26-SEP-2002.  
XX  
XX 01-MAR-2002; 2002WO-US005093.  
XX  
XX 16-MAR-2001; 2001US-0276596P.  
XX 13-APR-2001; 2001US-0283654P.  
XX 20-APR-2001; 2001US-0285238P.  
XX 03-MAY-2001; 2001US-0288548P.  
XX 11-MAY-2001; 2001US-0290351P.  
XX  
XX (ELIL) LILLY & CO ELI.  
XX  
XX Amegadzie BY, Basinski MB, Chen D, Huang C, Keleher GP;  
PI Perkins DR, Rostock PRJ, Rowlinson SW, Sankhavaram PR, Seno ET;  
PI Su EW, Zhi Y;  
XX  
XX WPI; 2003-018798/01.  
XX  
XX New mammalian LP polynucleotides and proteins, useful in gene therapy,  
PT e.g. for treating or preventing cancers, autoimmune (e.g. AIDS),  
PT cardiovascular (e.g. myocardial infarction) or neurological (e.g. stroke)  
PT disorders.  
XX  
XX Claim 18; Page 286-287; 290pp; English.  
XX  
XX The present invention relates to LP (LP318a, LP318b, LP288, LP289, LP343,  
CC LP319a, LP319b, LP321, LP317, LP283, LP344, LP345 or LP346) proteins and  
CC polynucleotides encoding such proteins. Sequences of the invention are  
CC used to diagnose, treat or prevent cell proliferative disorders (e.g.  
CC actinic keratinosis, arteriosclerosis, psoriasis, leukaemia, lymphoma,  
CC melanoma, brain cancer or breast cancer), autoimmune or inflammatory  
CC disorders (e.g. AIDS (acquired immune deficiency syndrome), Addison's  
CC disease, allergies, ankylosing spondylitis, amyloidosis, anaemia, asthma,  
CC Crohn's disease, Goodpasture's syndrome, gout, Hashimoto's thyroiditis or  
CC Grave's disease), cardiovascular disorders (e.g. congestive heart  
CC failure, ischaemic heart disease, angina pectoris, myocardial infarction,  
CC atherosclerosis or hypertension), neurological disorders (e.g. stroke,  
CC Parkinson's disease or Alzheimer's disease) or developmental disorders  
CC (e.g. Down's syndrome or cerebral palsy). They are also used in gene  
CC therapy. The present sequence is human LP283 splice variant protein,  
CC LP346  
XX  
XX Sequence 265 AA;  
SQ  
Query Match 59.4%; Score 43; DB 6; Length 265;  
Best Local Similarity 88.9%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CRPGQELTK 9  
|||||  
Db 184 CRPGFELTK 192  
RESULT 38  
AAU02951  
ID AAU02951 standard; protein; 389 AA.  
XX  
XX AAU02951;  
XX  
XX 12-SEP-2001 (first entry)  
DT

XX DE Angiotensin converting enzyme (ACEV) splice variant protein #51.

XX KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;

KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;

KW platelet-derived endothelial cell growth factor; cardiovascular disease;

KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;

KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;

KW myocardial infarction; coronary arterial thrombosis; renal disease;

KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;

KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;

KW nonarocidotic pulmonary granulomatous disease; endothelial abnormality;

XX KW vascular disorder; asbestosis.

OS Homo sapiens.

XX WO200136632-A2.

XX PD 25-MAY-2001.

XX PF 17-NOV-2000; 2000WO-IL000766.

XX PR 17-NOV-1999; 99IL-00132978.

XX PR 10-DEC-1999; 99IL-00133455.

XX PA (COMP-) COMPUGEN LTD.

XX PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;

XX DR WPI; 2001-336004/35.

XX DR N-PSDB; AAS06051.

XX PT Novel alternative splicing variants e.g. variant of angiotensin

PT converting enzyme (ACEV), useful in identifying candidate compounds

PT capable of binding to the variant and to detect anti-variant antibodies.

XX PS Claim 4; Fig 51; 519pp; English.

XX XX The sequence represents an angiotensin converting enzyme splice variant

CC (ACEV) polypeptide. The polypeptides of the invention include variants of

CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,

CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase

CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal

CC polypeptide receptor 2. The polypeptides and their associated nucleic

CC acids are useful for identification of variant sequences and detection of

CC candidate compounds capable of binding the molecules. The sequences of

CC the invention can be used in the treatment and diagnosis of various

CC disorders including cardiovascular diseases such as arteriosclerosis,

CC myocardial infarction and coronary arterial thrombosis, renal diseases

CC such as diabetic nephropathy, muscular diseases such as hypertrophy,

CC immune disorders such as immune complex nephritis, multiple sclerosis,

CC cancer, sarcoidosis, nonarocidotic pulmonary granulomatous diseases such

CC as asbestosis and vascular pathologies involving an endothelial

XX abnormality such as deep vein thrombosis

SQ Sequence 389 AA;

Query Match 69.4%; Score 43; DB 4; Length 389;

Best Local Similarity 72.7%; Pred. No. 30;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 367 CRPAQELQLQG 377

RESULT 39

AAG68259

ID AAG68259 standard; protein; 845 AA.

XX AC AAG68259;

XX DT 14-FEB-2002 (first entry)

XX DE Human POLY6 protein sequence SEQ ID NO:12.

XX KW Human; POLYX; gamma aminobutyric acid receptor; GABA receptor;

KW epidermal growth factor; EGF; complement receptor; HSPC; syntaxin;

KW haematopoietic stem and progenitor cell; sulphotransferase; prohibitin;

KW antidepressant; cerebroprotective; antiparkinsonian; nootropic; relaxant;

KW anticonvulsant; neuroleptic; neuroprotective; antialcoholic; cardiac;

KW tranquiliser; antiarrhythmic; psychiatric; medical; depression; stroke;

KW Parkinson's disease; Huntington's disease; Tourette's syndrome; anxiety;

KW amyotrophic lateral sclerosis; head trauma; Alzheimer's disease;

KW alcoholism; vigilance; muscle tension; epileptogenic; memory function;

KW cardiomyopathy; arrhythmogenic right ventricular dysplasia.

XX OS Homo sapiens.

XX WO200179294-A2.

XX PD 25-OCT-2001.

XX PF 19-APR-2001; 2001WO-US012854.

XX PR 19-APR-2000; 2000US-0198293P.

XX PR 20-APR-2000; 2000US-0198645P.

XX PR 25-APR-2000; 2000US-0199476P.

XX PR 26-APR-2000; 2000US-0199880P.

XX PR 26-APR-2000; 2000US-0200024P.

XX PR 26-APR-2000; 2000US-0200025P.

XX PR 09-JUN-2000; 2000US-0210809P.

XX PR 17-JUL-2000; 2000US-0218591P.

XX PR 11-AUG-2000; 2000US-0224610P.

XX PR 09-FEB-2001; 2001US-0267673P.

XX PR 27-FEB-2001; 2001US-0271814P.

XX PA (CURA-) CURAGEN CORP.

XX PI Taupier RJ, Vernet CAM, Fernandes E, Shimkets RA, Majumder K;

PI Padigaru M, Colman SD, Zerhusen BD, Spytek KA, Burgess CE, Liu X;

XX WPI; 2002-017601/02.

XX N-PSDB; ABA03875.

XX PT New isolated polypeptides for treating a broad range of pathological

PT states, e.g., depression, stroke, Parkinson's disease, Huntington's

PT disease, Tourette's syndrome, amyotrophic lateral sclerosis, head trauma,

PT and Alzheimer's.

XX Claim 1; Page 33-34; 155pp; English.

XX PS The present invention describes polypeptides (I), designated POLYX

XX polypeptides (e.g. POLY1, POLY2, etc.), and the polynucleotide sequences

CC (II) encoding them. POLY1-4 are members of the gamma aminobutyric acid

CC (GABA) receptor family; POLY5-8 are members of the epidermal growth

CC factor (EGF) family; POLY9-11 are members of the complement receptor

CC family; POLY12 is a member of the haematopoietic stem and progenitor cell

CC (HSPC) family; POLY13 is a member of the sulphotransferase family; POLY14

CC -16 are members of the syntaxin family; and POLY17 is a member of the

CC prohibitin family. (I) and (II) can have antidepressant,

CC cerebroprotective, antiparkinsonian, nootropic, relaxant, anticonvulsant,

CC neuroleptic, neuroprotective, antialcoholic, cardiac, tranquiliser and

CC antiarrhythmic activities. (I) and (II) can be used for treating or

CC preventing a POLYX-associated disorder in humans as a therapeutic in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease selected from a POLYX-associated disorder, for treating a

CC pathological state in a mammal, especially patients suffering from, e.g.,

CC psychiatric and medical conditions, depression, stroke, Parkinson's

CC disease, Huntington's disease, Tourette's syndrome, amyotrophic lateral

CC sclerosis, head trauma, Alzheimer's disease, alcoholism, vigilance,

CC anxiety, muscle tension, epileptogenic activity and memory functions,

CC cardiomyopathy and arrhythmogenic right ventricular dysplasia. The

XX present sequence represents POLY6

SQ Sequence 845 AA;

Query Match 69.4%; Score 43; DB 5; Length 845;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELTK 9  
|||  
Db 55 CRPGFELTK 63

## RESULT 40

ABU12092  
ID ABU12092 standard; protein; 845 AA.

AC ABU12092;

DT 17-FEB-2003 (first entry)

XX Novel human epidermal growth factor-like protein #2.

XX Gamma-aminobutyric acid receptor-like protein; depression; stroke;  
KW GABA receptor-like protein; Parkinson's disease; Huntington's disease;  
KW Tourette's syndrome; amyotrophic lateral sclerosis; head trauma;  
KW Alzheimer's disease; alcoholism; vigilance; anxiety; muscle tension;  
KW epileptogenic activity; memory; cardiomyopathy; cancer; angiogenesis;  
KW arrhythmogenic right ventricular dysplasia; renal disease; diabetes;  
KW Epidermal growth factor like protein; leukaemia; lupus; anaemia; ulcer;  
KW haematopoietic stem and progenitor cell like protein; cirrhosis;  
KW sulfotransferase-like protein; cholangitis; hepatitis; hyperthyroidism;  
KW developmental disorder; Syntaxin-like protein; myxoid liposarcoma;  
KW asthma; Lambert-Eaton myasthenic syndrome; acute myeloid leukaemia;  
KW transgenic animal.

XX Homo sapiens.

XX US2002123612-A1.

XX 05-SEP-2002.

XX 03-JUL-2001; 2001US-00898570.

XX 19-APR-2000; 2000US-0198293P.

XX 20-APR-2000; 2000US-0198645P.

XX 25-APR-2000; 2000US-0199476P.

XX 26-APR-2000; 2000US-0199880P.

XX 26-APR-2000; 2000US-0200024P.

XX 26-APR-2000; 2000US-0200025P.

XX 09-JUN-2000; 2000US-0210809P.

XX 03-JUL-2000; 2000US-0215855P.

XX 17-JUL-2000; 2000US-0218591P.

XX 11-AUG-2000; 2000US-0224610P.

XX 27-FEB-2001; 2001US-0271814P.

XX (GERL/) GERLACH V L.

XX (ELLE/) ELLERMAN K.

XX (MACD/) MACDOUGALL J R.

XX (SMIT/) SMITHSON G.

PI Gerlach VL, Ellerman K, Macdougall JR, Smithson G;

XX WPI; 2003-066815/06.

DR N-PSDB; ABX56471.

XX Novel polypeptides and nucleic acids which are members of epidermal  
PT growth factor, complement receptor families for diagnosing and treating  
PT psychiatric conditions, depression, stroke, Alzheimer's and Parkinson's  
PT disease.

XX Claim 1; Page 20-21; 91pp; English.

XX The invention describes an isolated POLYX (POLY1-17) polypeptide and its  
CC variant. POLYX polypeptides (especially POLY5, POLY6 and POLY7), the  
CC polynucleotides encoding them (I) and an anti-POLYX-antibody (III) are

CC useful for treating or preventing a pathology associated with POLYX  
CC polypeptide in humans and for treating a syndrome associated with human  
CC disease. POLYX polypeptide is also useful for identifying an agent that  
CC binds to POLYX and a cell expressing POLYX is useful for identifying a  
CC therapeutic agent for use in treatment of a pathology related to aberrant  
CC expression or physiological interactions of the polypeptide. (III) is  
CC useful for treating a pathological state in a mammal and for determining  
CC the presence or amount of POLYX in a sample. POLY1-4 (GABA receptor-like  
CC proteins) are useful for the treatment of psychiatric and medical  
CC conditions, depression, stroke, Parkinson's disease, Huntington's  
CC disease, Tourette's syndrome, amyotrophic lateral sclerosis, head trauma,  
CC Alzheimer's disease, alcoholism, vigilance, anxiety, muscle tension,  
CC epileptogenic activity and memory functions, cardiomyopathy and  
CC arrhythmogenic right ventricular dysplasia. POLY5-8 (Epidermal growth  
CC factor like proteins) may be useful for treating cancer, aberrant  
CC angiogenesis, renal disease and diabetes. POLY12 (haematopoietic stem and  
CC progenitor cell like protein) may be useful for treatment of leukaemia,  
CC lupus and anaemia. POLY13 (sulfotransferase-like protein) may be useful  
CC for treating cirrhosis, cholangitis, hepatitis, ulcers, hyperthyroidism  
CC and developmental disorders. POLY14-16 (Syntaxin-like proteins) may be  
CC useful in treatment of Lambert-Eaton myasthenic syndrome, asthma, myxoid  
CC liposarcoma and acute myeloid leukaemia, and POLY 18 may be useful in  
CC treatment of cancers. Cells comprising (I) are useful for producing non-  
CC human transgenic animals which are useful for studying the function  
CC and/or activity of POLYX protein and for identifying and/or evaluating  
CC modulators of POLYX protein activity. This is the amino acid sequence of  
XX a novel human protein

SQ Sequence 845 AA;

Query Match 69.4%; Score 43; DB 6; Length 845;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9

Db 55 CRPGFELTK 63

Search completed: May 5, 2004, 14:38:04  
Job time : 5.46233 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:35:32 ; Search time 1.58219 Seconds  
(without alignments)  
358.923 Million cell updates/sec

Title: US-10-067-122B-2\_COPY\_105\_115

Perfect score: 62

Sequence: 1 CRPQELTKQG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	62	100.0	11	4	US-08-012-269A-13
2	62	100.0	191	3	US-08-974-022-52
3	62	100.0	191	3	US-08-795-445A-52
4	62	100.0	191	3	US-08-795-447A-52
5	62	100.0	191	3	US-08-974-186-52
6	62	100.0	191	3	US-08-795-446B-52
7	62	100.0	191	4	US-08-706-945D-139
8	62	100.0	191	4	US-08-577-788C-53
9	62	100.0	256	1	US-08-236-918A-6
10	62	100.0	256	4	US-09-150-864A-6
11	62	100.0	256	4	US-08-012-269A-2
12	62	100.0	256	4	US-09-623-545A-3
13	62	100.0	256	5	PCT-US96-03965-2
14	57	91.9	12	4	US-08-012-269A-7
15	47	75.8	132	4	US-09-523-323-55
16	47	75.8	219	2	US-08-816-605-2
17	47	75.8	255	1	US-08-236-918A-8
18	47	75.8	255	2	US-08-816-605-9
19	47	75.8	255	3	US-09-006-353A-11
20	47	75.8	255	4	US-09-007-097-2
21	47	75.8	255	4	US-09-150-864A-8
22	47	75.8	255	4	US-09-573-986-11
23	47	75.8	255	4	US-09-578-764A-2
24	47	75.8	255	4	US-09-623-545A-2
25	47	75.8	255	5	PCT-US96-03965-8
26	41	66.1	135	4	US-09-746-359A-70
27	41	66.1	196	4	US-09-746-359A-67

28	41	66.1	201	4	US-09-746-359A-59	Sequence 59, Appl
29	41	66.1	203	4	US-09-746-359A-15	Sequence 15, Appl
30	41	66.1	307	4	US-09-746-359A-58	Sequence 58, Appl
31	41	66.1	311	4	US-09-746-359A-14	Sequence 14, Appl
32	41	66.1	336	4	US-09-746-359A-57	Sequence 57, Appl
33	40	64.5	297	4	US-09-548-130-6	Sequence 6, Appl
34	40	64.5	299	4	US-09-548-130-3	Sequence 3, Appl
35	40	64.5	299	4	US-10-119-466-12	Sequence 12, Appl
36	39	62.9	228	3	US-08-911-423-2	Sequence 2, Appl
37	39	62.9	228	4	US-09-512-363-7	Sequence 7, Appl
38	39	62.9	228	4	US-09-176-200-7	Sequence 7, Appl
39	37	59.7	151	3	US-09-286-529-4	Sequence 4, Appl
40	37	59.7	210	3	US-09-286-529-3	Sequence 3, Appl
41	37	59.7	504	4	US-09-252-991A-28279	Sequence 28279, A
42	37	59.7	1102	4	US-09-358-383C-36	Sequence 36, Appl
43	37	59.7	1107	4	US-09-358-383C-16	Sequence 16, Appl
44	36.5	58.9	59	4	US-09-461-325-481	Sequence 481, App
45	36.5	58.9	59	4	US-10-012-542-481	Sequence 481, App

ALIGNMENTS

RESULT 1  
US-08-012-269A-13  
; Sequence 13, Application US/08012269A  
; Patent No. 6362325  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung S.  
; TITLE OF INVENTION: MURINE 4-1BB GENE  
; FILE REFERENCE: 740.009US1  
; CURRENT APPLICATION NUMBER: US/08/012,269A  
; CURRENT FILING DATE: 1993-02-01  
; PRIOR APPLICATION NUMBER: US 07/922,996  
; PRIOR FILING DATE: 1992-07-30  
; PRIOR APPLICATION NUMBER: US 07/267,572  
; PRIOR FILING DATE: 1988-11-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-012-269A-13

Query Match 100.0%; Score 62; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CRPQELTKQG 11  
| | | | | | | | | | | |  
Db 1 CRPQELTKQG 11

RESULT 2  
US-08-974-022-52  
; Sequence 52, Application US/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, Willaim J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/974,022  
;; FILING DATE: 12-DEC-1995  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/577,788  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Winter, Robert B.  
;; REFERENCE/DOCKET NUMBER: A-378  
;; INFORMATION FOR SEQ ID NO: 52:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 191 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-974-022-52

Query Match 100.0%; Score 62; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115

## RESULT 3

US-08-795-445A-52  
; Sequence 52, Application US/08795445A  
; Patent No. 628485

;; GENERAL INFORMATION:  
;; APPLICANT: Boyle, William J.  
;; APPLICANT: Lacey, David L.  
;; APPLICANT: Calzone, Frank J.  
;; APPLICANT: Chang, Ming-Shi  
;; TITLE OF INVENTION: OSTEOPROTEGERIN  
;; NUMBER OF SEQUENCES: 53  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Amgen Inc.  
;; STREET: 1840 Dehavilland Drive  
;; CITY: Thousand Oaks  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 91320-1789  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/795,445A  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/577,788  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Winter, Robert B.  
;; REFERENCE/DOCKET NUMBER: A-378  
;; INFORMATION FOR SEQ ID NO: 52:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 191 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-795-445A-52

Query Match 100.0%; Score 62; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115

## RESULT 4

US-08-795-447A-52  
; Sequence 52, Application US/08795447A  
; Patent No. 6284728

;; GENERAL INFORMATION:  
;; APPLICANT: Boyle, William J.  
;; APPLICANT: Lacey, David L.  
;; APPLICANT: Calzone, Frank J.  
;; APPLICANT: Chang, Ming-Shi  
;; TITLE OF INVENTION: Osteoprotegerin  
;; NUMBER OF SEQUENCES: 53  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Amgen Inc.  
;; STREET: One Amgen Center Drive  
;; CITY: Thousand Oaks  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 91362-1789

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/795,447A  
;; FILING DATE:  
;; CLASSIFICATION: 514

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Winter, Robert B.  
;; REFERENCE/DOCKET NUMBER: A-378D2  
;; INFORMATION FOR SEQ ID NO: 52:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 191 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-795-447A-52

Query Match 100.0%; Score 62; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115

## RESULT 5

US-08-974-186-52  
; Sequence 52, Application US/08974186  
; Patent No. 6284740

;; GENERAL INFORMATION:  
;; APPLICANT: Boyle, William J.  
;; APPLICANT: Lacey, David L.  
;; APPLICANT: Calzone, Frank J.  
;; APPLICANT: Chang, Ming-Shi  
;; TITLE OF INVENTION: OSTEOPROTEGERIN  
;; NUMBER OF SEQUENCES: 53  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Amgen Inc.  
;; STREET: 1840 Dehavilland Drive  
;; CITY: Thousand Oaks

STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,186  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-186-52

Query Match 100.0%; Score 62; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|||  
Db 105 CRPGQELTKQG 115

## RESULT 6

US-08-795-446B-52  
Sequence 52, Application US/08795446B  
Patent No. 6288032  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,446B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-446B-52

Query Match 100.0%; Score 62; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|||  
Db 105 CRPGQELTKQG 115

## RESULT 7

US-08-706-945D-139  
Sequence 139, Application US/08706945D  
Patent No. 6369027  
GENERAL INFORMATION:  
APPLICANT: Boyle, William  
APPLICANT: Lacey, David  
APPLICANT: Calzone, Frank  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
FILE REFERENCE: A-378CIP  
CURRENT APPLICATION NUMBER: US/08/706,945D  
CURRENT FILING DATE: 1996-09-03  
PRIOR APPLICATION NUMBER: 08/577,788  
PRIOR FILING DATE: 1995-12-22  
NUMBER OF SEQ ID NOS: 145  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 139  
LENGTH: 191  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-706-945D-139

Query Match 100.0%; Score 62; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|||  
Db 105 CRPGQELTKQG 115

## RESULT 8

US-08-577-788C-53  
Sequence 53, Application US/08577788C  
Patent No. 6613544  
GENERAL INFORMATION:  
APPLICANT: Boyle, William  
APPLICANT: Lacey, David  
APPLICANT: Calzone, Frank  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
FILE REFERENCE: A-378 Rev  
CURRENT APPLICATION NUMBER: US/08/577,788C  
CURRENT FILING DATE: 1995-12-22  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 53  
LENGTH: 191  
TYPE: PRT  
ORGANISM: Mus musculus  
US-08-577-788C-53

Query Match 100.0%; Score 62; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|||

Db 105 CRPGQELTKQG 115

RESULT 9

US-08-236-918A-6

; Sequence 6, Application US/08236918A

; Patent No. 5674704

; GENERAL INFORMATION:

; APPLICANT: Alderson, Mark R.

; APPLICANT: Goodwin, Raymond G.

; APPLICANT: Smith, Craig A.

; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple 7.5.3

; SOFTWARE: Microsoft Word, Version #6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/236,918A

; FILING DATE: 06-May-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/060,843

; FILING DATE: 07-May-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Anderson, Kathryn A.

; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2801-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 256 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-236-918A-6

Query Match 100.0%; Score 62; DB 1; Length 256;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 105 CRPGQELTKQG 115

RESULT 10

US-09-150-864A-6

; Sequence 6, Application US/09150864A

; Patent No. 6355779

; GENERAL INFORMATION:

; APPLICANT: Alderson, Mark R.

; APPLICANT: Goodwin, Raymond G.

; APPLICANT: Smith, Craig A.

; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor

; TITLE OF INVENTION: That Binds Thereto

; FILE REFERENCE: 2801-B

; CURRENT APPLICATION NUMBER: US/09/150,864A

; CURRENT FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 08/060,843

; PRIOR FILING DATE: 1993-05-07

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 256

; TYPE: PRT

; ORGANISM: Mus sp. (clone: mu4-1BB)

US-09-150-864A-6

Query Match 100.0%; Score 62; DB 4; Length 256;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 105 CRPGQELTKQG 115

RESULT 11

US-08-012-269A-2

; Sequence 2, Application US/08012369A

; Patent No. 6362325

; GENERAL INFORMATION:

; APPLICANT: Kwon, Byoung S.

; TITLE OF INVENTION: MURINE 4-1BB GENE

; FILE REFERENCE: 740.009US1

; CURRENT APPLICATION NUMBER: US/08/012,269A

; CURRENT FILING DATE: 1993-02-01

; PRIOR APPLICATION NUMBER: US 07/922,996

; PRIOR FILING DATE: 1992-07-30

; PRIOR APPLICATION NUMBER: US 07/267,572

; PRIOR FILING DATE: 1988-11-07

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version. 4.0

; SEQ ID NO 2

; LENGTH: 256

; TYPE: PRT

; ORGANISM: Mus musculus

US-08-012-269A-2

Query Match 100.0%; Score 62; DB 4; Length 256;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

Db 105 CRPGQELTKQG 115

RESULT 12

US-09-623-545A-3

; Sequence 3, Application US/09623545A

; Patent No. 6627200

; GENERAL INFORMATION:

; APPLICANT: Merckle GmbH

; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE

; TITLE OF INVENTION: PROLIFERATION OF PERIPHERAL MONOCYTES

; FILE REFERENCE: 30424.1USWO

; CURRENT APPLICATION NUMBER: US/09/623,545A

; CURRENT FILING DATE: 2000-09-05

; PRIOR APPLICATION NUMBER: EPO 98103859.9

; PRIOR FILING DATE: 1999-03-05

; PRIOR APPLICATION NUMBER: PCT/EP99/01440

; PRIOR FILING DATE: 1999-03-05

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 256

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-623-545A-3

Query Match 100.0%; Score 62; DB 4; Length 256;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115

RESULT 13  
PCT-US96-03965-2  
; Sequence 2, Application PC/TUS9603965  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung Se  
; APPLICANT: Kang, Chang-Yuil  
; TITLE OF INVENTION: Monoclonal antibody against human  
; TITLE OF INVENTION: receptor 4-1BB  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Barnard, Brown & Michaels  
; STREET: 306 East State Street, Suite 220  
; CITY: Ithaca  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 14850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/03965  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/122,796  
; FILING DATE: 16-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,269  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/922,996  
; FILING DATE: 30-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/267,577  
; FILING DATE: 07-NOV-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michaels, Christopher A  
; REGISTRATION NUMBER: 34,390  
; REFERENCE/DOCKET NUMBER: KW05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 607-273-1711  
; TELEFAX: 607-273-2609  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-03965-2

Query Match 100.0%; Score 62; DB 5; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115

RESULT 14  
US-08-012-269A-7  
; Sequence 7, Application US/08012269A  
; Patent No. 6362325  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung S.

; TITLE OF INVENTION: MURINE 4-1BB GENE  
; FILE REFERENCE: 740.009US1  
; CURRENT APPLICATION NUMBER: US/08/012,269A  
; CURRENT FILING DATE: 1993-02-01  
; PRIOR APPLICATION NUMBER: US 07/922,996  
; PRIOR FILING DATE: 1992-07-30  
; PRIOR APPLICATION NUMBER: US 07/267,572  
; PRIOR FILING DATE: 1988-11-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: An artificial peptide  
US-08-012-269A-7

Query Match 91.9%; Score 57; DB 4; Length 12;  
Best Local Similarity 90.9%; Pred. No. 0.00069;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
Db 1 CRPGQELTKSG 11

RESULT 15  
US-09-523-323-55  
; Sequence 55, Application US/09523323  
; Patent No. 6635743  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Ullrich, Stephen  
; APPLICANT: Zhai, Yifan  
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
; FILE REFERENCE: 1488.065000C  
; CURRENT APPLICATION NUMBER: US/09/523,323  
; CURRENT FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/168,380  
; EARLIER FILING DATE: 1999-12-02  
; EARLIER APPLICATION NUMBER: 60/148,326  
; EARLIER FILING DATE: 1999-08-11  
; EARLIER APPLICATION NUMBER: 60/142,657  
; EARLIER FILING DATE: 1999-07-06  
; EARLIER APPLICATION NUMBER: 60/137,457  
; EARLIER FILING DATE: 1999-06-04  
; EARLIER APPLICATION NUMBER: 60/124,041  
; EARLIER FILING DATE: 1999-03-11  
; EARLIER APPLICATION NUMBER: 09/252,656  
; EARLIER FILING DATE: 1999-02-19  
; EARLIER APPLICATION NUMBER: 60/075,409  
; EARLIER FILING DATE: 1998-02-20  
; EARLIER APPLICATION NUMBER: 09/027,287  
; EARLIER FILING DATE: 1998-02-20  
; EARLIER APPLICATION NUMBER: 09/003,886  
; EARLIER FILING DATE: 1998-01-07  
; EARLIER APPLICATION NUMBER: 08/822,953  
; EARLIER FILING DATE: 1997-03-21  
; EARLIER APPLICATION NUMBER: 60/013,923  
; EARLIER FILING DATE: 1996-03-22  
; EARLIER APPLICATION NUMBER: 60/030,157  
; EARLIER FILING DATE: 1996-10-31  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-523-323-55

Query Match 75.8%; Score 47; DB 4; Length 132;  
Best Local Similarity 72.7%; Pred. No. 0.49;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|: |||||:  
Db 79 CKQGQELTKKG 89

## RESULT 16

US-08-816-605-2  
; Sequence 2, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,605  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8512  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 219 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-816-605-2

Query Match 75.8%; Score 47; DB 2; Length 219;  
Best Local Similarity 72.7%; Pred. No. 0.83;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|: |||||:  
Db 70 CKQGQELTKKG 80

## RESULT 17

US-08-236-918A-8  
; Sequence 8, Application US/08236918A  
; Patent No. 5674704  
; GENERAL INFORMATION:  
; APPLICANT: Alderson, Mark R.  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; TITLE OF INVENTION: Cytokine Designated 4-IBB Ligand  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle

; STATE: Washington  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple 7.5.3  
; SOFTWARE: Microsoft Word, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,918A  
; FILING DATE: 06-May-1994  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/060,843  
; FILING DATE: 07-May-1993  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:  
; NAME: Anderson, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2801-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 587-0430  
; TELEFAX: (206) 233-0644  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-236-918A-8

Query Match 75.8%; Score 47; DB 1; Length 255;  
Best Local Similarity 72.7%; Pred. No. 0.97;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|: |||||:  
Db 106 CKQGQELTKKG 116

## RESULT 18

US-08-816-605-9  
; Sequence 9, Application US/08816605  
; Patent No. 5874240  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/816,605  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8512

```
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 255 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-816-605-9
Query Match          75.8%; Score 47; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 19
US-09-006-353A-11
; Sequence 11, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 255 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-006-353A-11
Query Match          75.8%; Score 47; DB 3; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 20
US-09-007-097-2
; Sequence 2, Application US/09007097A
```

```
; Patent No. 6303121
; GENERAL INFORMATION:
; APPLICANT: KWON, BYOUNG
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/007,097A
; CURRENT FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-007-097-2
Query Match          75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 21
US-09-150-864A-8
; Sequence 8, Application US/09150864A
; Patent No. 6355779
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark R.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand and Human Receptor
; TITLE OF INVENTION: That Binds Thereto
; FILE REFERENCE: 2801-B
; CURRENT APPLICATION NUMBER: US/09/150,864A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/060,843
; PRIOR FILING DATE: 1993-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens (clone: hu4-13B)
US-09-150-864A-8
Query Match          75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 22
US-09-573-986-11
; Sequence 11, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.128004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 255
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```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-573-986-11

Query Match      75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 23
US-09-578-764A-2
; Sequence 2, Application US/09578764A
; Patent No. 6569997
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; TITLE OF INVENTION: METHOD OF USING HUMAN RECEPTOR PROTEIN 4-1BB
; FILE REFERENCE: 740.011US1
; CURRENT APPLICATION NUMBER: US/09/578,764A
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-578-764A-2

Query Match      75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 24
US-09-623-545A-2
; Sequence 2, Application US/09623545A
; Patent No. 6627200
; GENERAL INFORMATION:
; APPLICANT: Merckle GmbH
; TITLE OF INVENTION: UTILIZATION OF CD137 IN ORDER TO PROMOTE THE
; FILE REFERENCE: 30424.1USWO
; CURRENT APPLICATION NUMBER: US/09/623,545A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: EPO 98103859.9
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/EP99/01440
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-623-545A-2

Query Match      75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 25
US-09-623-545A-2

Query Match      75.8%; Score 47; DB 4; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

PCT-US96-03965-8
; Sequence 8, Application PC/TUS9603965
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; APPLICANT: Kang, Chang-Yuil
; TITLE OF INVENTION: Monoclonal antibody against human
; TITLE OF INVENTION: receptor 4-1BB
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnard, Brown & Michaels
; STREET: 306 East State Street, Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03965
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,796
; FILING DATE: 16-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,269
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,996
; FILING DATE: 30-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/267,577
; FILING DATE: 07-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: KW05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-03965-8

Query Match      75.8%; Score 47; DB 5; Length 255;
Best Local Similarity 72.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 26
US-09-746-359A-70
; Sequence 70, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
```

```
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-70
```

```
Query Match 66.1%; Score 41; DB 4; Length 135;
Best Local Similarity 70.0%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 RPQELTKQG 11
    |||||:|
Db 52 RFGMEITKDG 61
```

```
RESULT 27
US-09-746-359A-67
; Sequence 67, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-67
```

```
Query Match 66.1%; Score 41; DB 4; Length 196;
Best Local Similarity 70.0%; Pred. No. 8.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 RPQELTKQG 11
    |||||:|
Db 106 RFGMEITKDG 115
```

```
RESULT 28
US-09-746-359A-59
; Sequence 59, Application US/09746359A
; Patent No. 6610286
```

```
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-59
```

```
Query Match 66.1%; Score 41; DB 4; Length 201;
Best Local Similarity 70.0%; Pred. No. 8.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 RPQELTKQG 11
    |||||:|
Db 111 RFGMEITKDG 120
```

```
RESULT 29
US-09-746-359A-15
; Sequence 15, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-15
```

```
Query Match 66.1%; Score 41; DB 4; Length 203;
Best Local Similarity 70.0%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 RPQQLTKQG 11
      ||| |:|||
Db      111 RFGMEITKDG 120

RESULT 30
US-09-746-359A-58
; Sequence 58, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-58

Query Match      66.1%; Score 41; DB 4; Length 307;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY      2 RPQQLTKQG 11
      ||| |:|||
Db      111 RFGMEITKDG 120

RESULT 31
US-09-746-359A-14
; Sequence 14, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
```

```
QY      2 RPQQLTKQG 11
      ||| |:|||
Db      140 RFGMEITKDG 149

Query Match      66.1%; Score 41; DB 4; Length 311;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY      2 RPQQLTKQG 11
      ||| |:|||
Db      140 RFGMEITKDG 149

RESULT 32
US-09-746-359A-57
; Sequence 57, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-57

Query Match      66.1%; Score 41; DB 4; Length 336;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY      2 RPQQLTKQG 11
      ||| |:|||
Db      140 RFGMEITKDG 149

RESULT 33
US-09-548-130-6
; Sequence 6, Application US/09548130
; Patent No. 6534061
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Pan, James
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND
; FILE REFERENCE: PI739R1
; CURRENT APPLICATION NUMBER: US/09/548,130
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: US 60/128,849
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 297
```

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
Db 21 CGPGQELSK 29

RESULT 36  
US-08-911-423-2  
; Sequence 2, Application US/08911423  
; Patent No. 6111090  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Randall, Troy D.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
; TITLE OF INVENTION: REAGENTS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/911,423  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/023,419  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/027,901  
; FILING DATE: 07-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0612K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-9196  
; TELEFAX: 650-496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 228 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-911-423-2

Query Match 62.9%; Score 39; DB 3; Length 228;  
Best Local Similarity 54.5%; Pred. No. 23;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11  
Db 82 CQPGQVESQ 92

RESULT 37  
US-09-512-363-7  
; Sequence 7, Application US/09512363  
; Patent No. 6503184  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins  
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2

TYPE: PRT  
; ORGANISM: Human  
US-09-548-130-6

Query Match 64.5%; Score 40; DB 4; Length 297;  
Best Local Similarity 77.8%; Pred. No. 20;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
Db 21 CGPGQELSK 29

RESULT 34  
US-09-548-130-3  
; Sequence 3, Application US/09548130  
; Patent No. 6534061  
; GENERAL INFORMATION:  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Pan, James  
; APPLICANT: Yan, Minhong  
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME  
; FILE REFERENCE: P1739R1  
; CURRENT APPLICATION NUMBER: US/09/548,130  
; CURRENT FILING DATE: 2000-04-12  
; EARLIER APPLICATION NUMBER: US 60/128,849  
; EARLIER FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 3  
; LENGTH: 299  
; TYPE: PRT  
; ORGANISM: Human  
US-09-548-130-3

Query Match 64.5%; Score 40; DB 4; Length 299;  
Best Local Similarity 77.8%; Pred. No. 20;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
Db 21 CGPGQELSK 29

RESULT 35  
US-10-119-466-12  
; Sequence 12, Application US/10119466  
; Patent No. 6607899  
; GENERAL INFORMATION:  
; APPLICANT: Chui, Clarissa  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Milton, Sean  
; APPLICANT: Yan, Minhong  
; APPLICANT: Yi, Sothy  
; TITLE OF INVENTION: CLONING METHOD  
; FILE REFERENCE: P1797  
; CURRENT APPLICATION NUMBER: US/10/119,466  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: US/09/480,782  
; PRIOR FILING DATE: 2000-01-10  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 12  
; LENGTH: 299  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Homo sapiens  
; LOCATION: 1-299  
; OTHER INFORMATION:  
; US-10-119-466-12

Query Match 64.5%; Score 40; DB 4; Length 299;  
Best Local Similarity 77.8%; Pred. No. 20;

```
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/512,363
; CURRENT FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: 60/063,212
; EARLIER FILING DATE: 1997-10-21
; EARLIER APPLICATION NUMBER: 09/176,200
; EARLIER FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 60/121,648
; EARLIER FILING DATE: 1999-02-24
; EARLIER APPLICATION NUMBER: 60/134,172
; EARLIER FILING DATE: 1999-05-13
; EARLIER APPLICATION NUMBER: 60/144,076
; EARLIER FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-512-363-7

Query Match      62.9%; Score 39; DB 4; Length 228;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      82 CQPGQRVESQG 92

RESULT 38
US-09-176-200-7
; Sequence 7, Application US/09176200
; Patent No. 6509173
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/176,200
; CURRENT FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 60/063,212
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-176-200-7

Query Match      62.9%; Score 39; DB 4; Length 228;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      82 CQPGQRVESQG 92

RESULT 39
US-09-286-529-4
; Sequence 4, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 151
; TYPE: PRT
; ORGANISM: human
US-09-286-529-4

Query Match      59.7%; Score 37; DB 3; Length 151;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CRPGQELTKQ 10
Db      53 CGPGMELSKE 62

RESULT 40
US-09-286-529-3
; Sequence 3, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 210
; TYPE: PRT
; ORGANISM: human
US-09-286-529-3

Query Match      59.7%; Score 37; DB 3; Length 210;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CRPGQELTKQ 10
Db      52 CGPGMELSKE 61

Search completed: May 5, 2004, 14:42:16
Job time : 1.58219 secs
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:40:42 ; Search time 4.06849 Seconds  
(without alignments)  
749.438 Million cell updates/sec

Title: US-10-067-122B-2\_COPY\_105\_115  
Perfect score: 62  
Sequence: 1 CRPGQELTKQG 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues 1138120

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	62	100.0	11	14	US-10-067-122-13
2	62	100.0	191	11	US-09-405-032-136
3	62	100.0	256	13	US-10-027-199-10
4	62	100.0	256	14	US-10-067-122-2
5	57	91.9	12	14	US-10-067-122-7
6	47	75.8	132	15	US-10-375-680-55
7	47	75.8	219	9	US-09-739-394-2
8	47	75.8	219	13	US-10-097-330-2
9	47	75.8	255	9	US-09-739-394-9
10	47	75.8	255	9	US-09-826-212-11
11	47	75.8	255	9	US-09-935-727-13
12	47	75.8	255	10	US-09-877-336-2
13	47	75.8	255	13	US-10-097-330-9
14	47	75.8	255	13	US-10-027-199-2
15	47	75.8	255	14	US-10-170-997-2

16	47	75.8	255	14	US-10-186-643-11	Sequence 11, Appl
17	47	75.8	255	14	US-10-207-655-160	Sequence 160, Appl
18	47	75.8	255	15	US-10-418-242-13	Sequence 13, Appl
19	43	69.4	845	9	US-09-898-570-12	Sequence 12, Appl
20	43	69.4	845	10	US-09-839-446-12	Sequence 12, Appl
21	43	69.4	880	15	US-10-104-047-2834	Sequence 2834, Ap
22	43	69.4	897	14	US-10-239-663-35	Sequence 35, Appl
23	43	69.4	914	15	US-10-406-073-6	Sequence 6, Appl
24	43	69.4	974	9	US-09-898-570-14	Sequence 14, Appl
25	43	69.4	974	10	US-09-839-446-14	Sequence 14, Appl
26	43	69.4	993	14	US-10-239-663-36	Sequence 36, Appl
27	43	69.4	993	15	US-10-406-073-8	Sequence 8, Appl
28	43	69.4	993	15	US-10-406-073-15	Sequence 15, Appl
29	43	69.4	1006	11	US-09-930-512-18	Sequence 18, Appl
30	43	69.4	1009	9	US-09-898-570-16	Sequence 16, Appl
31	43	69.4	1009	10	US-09-839-446-16	Sequence 16, Appl
32	41	66.1	15	14	US-10-220-033-38	Sequence 38, Appl
33	41	66.1	135	9	US-09-746-359A-70	Sequence 70, Appl
34	41	66.1	135	15	US-10-424-658-70	Sequence 67, Appl
35	41	66.1	196	9	US-09-746-359A-67	Sequence 67, Appl
36	41	66.1	196	15	US-10-424-658-67	Sequence 59, Appl
37	41	66.1	201	9	US-09-746-359A-59	Sequence 16, Appl
38	41	66.1	201	9	US-09-912-672A-16	Sequence 35, Appl
39	41	66.1	201	10	US-09-925-055D-35	Sequence 59, Appl
40	41	66.1	201	15	US-10-424-658-59	Sequence 15, Appl
41	41	66.1	203	9	US-09-746-359A-15	Sequence 15, Appl
42	41	66.1	203	12	US-09-951-268-6	Sequence 6, Appl
43	41	66.1	203	15	US-10-424-658-15	Sequence 15, Appl
44	41	66.1	229	14	US-10-233-873A-2	Sequence 2, Appl
45	41	66.1	282	9	US-09-912-672A-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-10-067-122-13  
; Sequence 13, Application US/10067122  
; Publication No. US20030100745A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung S.  
; TITLE OF INVENTION: MURINE 4-LBB GENE  
; FILE REFERENCE: 740.009US1  
; CURRENT APPLICATION NUMBER: US/10/067,122  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 08/012,269  
; PRIOR FILING DATE: 1993-02-01  
; PRIOR APPLICATION NUMBER: US 07/922,996  
; PRIOR FILING DATE: 1992-07-30  
; PRIOR APPLICATION NUMBER: US 07/267,572  
; PRIOR FILING DATE: 1988-11-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-067-122-13

Query Match 100.0%; Score 62; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00027;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
| | | | | | | | | |  
Db 1 CRPGQELTKQG 11

RESULT 2  
US-09-405-032-136  
; Sequence 136, Application US/09405032  
; Publication No. US20030207827A1  
; GENERAL INFORMATION:

APPLICANT: Amgen Inc.  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 168  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 DeHavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: United States  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/405,032  
FILING DATE: 24-Sep-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378-CIP2  
INFORMATION FOR SEQ ID NO: 136:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 136:  
US-09-405-032-136

Query Match 100.0%; Score 62; DB 11; Length 191;  
Best Local Similarity 100.0%; Pred. No. 0.0055;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
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Db 105 CRPGQELTKQG 115

RESULT 3  
US-10-027-199-10  
; Sequence 10, Application US/10027199  
; Publication No. US20020168719A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung  
; TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND METHODS  
; FILE REFERENCE: 740.013US2  
; CURRENT APPLICATION NUMBER: US/10/027,199  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652  
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/122,796  
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-027-199-10

Query Match 100.0%; Score 62; DB 13; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0075;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|||||  
Db 105 CRPGQELTKQG 115

RESULT 4  
US-10-067-122-2  
; Sequence 2, Application US/10067122  
; Publication No. US20030100745A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung S.  
; TITLE OF INVENTION: MURINE 4-1BB GENE  
; FILE REFERENCE: 740.009US1  
; CURRENT APPLICATION NUMBER: US/10/067,122  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 08/012,269  
; PRIOR FILING DATE: 1993-02-01  
; PRIOR APPLICATION NUMBER: US 07/922,996  
; PRIOR FILING DATE: 1992-07-30  
; PRIOR APPLICATION NUMBER: US 07/267,572  
; PRIOR FILING DATE: 1988-11-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-067-122-2

Query Match 100.0%; Score 62; DB 14; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0075;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|||||  
Db 105 CRPGQELTKQG 115

RESULT 5  
US-10-067-122-7  
; Sequence 7, Application US/10067122  
; Publication No. US20030100745A1  
; GENERAL INFORMATION:  
; APPLICANT: Kwon, Byoung S.  
; TITLE OF INVENTION: MURINE 4-1BB GENE  
; FILE REFERENCE: 740.009US1  
; CURRENT APPLICATION NUMBER: US/10/067,122  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 08/012,269  
; PRIOR FILING DATE: 1993-02-01  
; PRIOR APPLICATION NUMBER: US 07/922,996  
; PRIOR FILING DATE: 1992-07-30  
; PRIOR APPLICATION NUMBER: US 07/267,572  
; PRIOR FILING DATE: 1988-11-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: An artificial peptide  
US-10-067-122-7

Query Match 91.9%; Score 57; DB 14; Length 12;  
Best Local Similarity 90.9%; Pred. No. 0.0023;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|||||  
Db 1 CRPGQELTKSG 11

RESULT 6  
US-10-375-680-55  
; Sequence 55, Application US/10375680

Publication No. US20040009147A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ruben, Steven M  
; APPLICANT: Ullrich, Stephen  
; APPLICANT: Zhai, Yifan  
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
; FILE REFERENCE: 1488.065000E  
; CURRENT APPLICATION NUMBER: US/10/375,680  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,234  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-375-680-55

Query Match 75.8%; Score 47; DB 15; Length 132;  
Best Local Similarity 72.7%; Pred. No. 1.7;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 79 CKQGQELTKKG 89

RESULT 7  
US-09-739-394-2  
; Sequence 2, Application US/09739394  
; Patent No. US20010014465A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; Yu, Guo-Liang  
; Gentz, Reiner  
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/739,394  
; FILING DATE: 19-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/253,549  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8512  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 219 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-739-394-2

Query Match 75.8%; Score 47; DB 9; Length 219;  
Best Local Similarity 72.7%; Pred. No. 2.9;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 70 CKQGQELTKKG 80

RESULT 8  
US-10-097-330-2  
; Sequence 2, Application US/10097330  
; Publication No. US20020127651A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT  
; FILE REFERENCE: PF254D1C2  
; CURRENT APPLICATION NUMBER: US/10/097,330  
; CURRENT FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 09/739,394  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/253,549  
; PRIOR FILING DATE: 1999-02-22  
; PRIOR APPLICATION NUMBER: US 08/816,605  
; PRIOR FILING DATE: 1997-03-13  
; PRIOR APPLICATION NUMBER: US 60/013,474  
; PRIOR FILING DATE: 1996-03-15  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-097-330-2

Query Match 75.8%; Score 47; DB 13; Length 219;  
Best Local Similarity 72.7%; Pred. No. 2.9;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 70 CKQGQELTKKG 80

RESULT 9  
US-09-739-394-9  
; Sequence 9, Application US/09739394  
; Patent No. US20010014465A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; Yu, Guo-Liang  
; Gentz, Reiner  
; TITLE OF INVENTION: Human 4-IBB Receptor Splicing Variant  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/739,394  
; FILING DATE: 19-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/253,549  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF254  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8512  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 219 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

APPLICATION NUMBER: 09/253,549  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF254  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-739-394-9

Query Match 75.8%; Score 47; DB 9; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.4;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

## RESULT 10

US-09-826-212-11  
Sequence 11, Application US/09826212  
Patent No. US20010021516A1  
GENERAL INFORMATION:  
APPLICANT: Wei, Ying-Fei  
APPLICANT: Gentz, Reiner  
APPLICANT: Ruben, Steven  
APPLICANT: Ni, Jian  
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
FILE REFERENCE: 1488.1280006  
CURRENT APPLICATION NUMBER: US/09/826,212  
CURRENT FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 11  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-826-212-11

Query Match 75.8%; Score 47; DB 9; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.4;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

## RESULT 11

US-09-935-727-13  
Sequence 13, Application US/09935727  
Patent No. US20020150583A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
FILE REFERENCE: PF454P2  
CURRENT APPLICATION NUMBER: US/09/935,727  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 60/303,224  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: 60/252,131  
PRIOR FILING DATE: 2000-11-21  
PRIOR APPLICATION NUMBER: 60/227,598

PRIOR FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: 09/518,931  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: 60/168,235  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 60/146,371  
PRIOR FILING DATE: 1999-08-02  
PRIOR APPLICATION NUMBER: 60/131,964  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: 60/131,270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/124,092  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/121,774  
PRIOR FILING DATE: 1999-03-04  
PRIOR APPLICATION NUMBER: 09/006,352  
PRIOR FILING DATE: 1998-01-13  
PRIOR APPLICATION NUMBER: 60/035,496  
PRIOR FILING DATE: 1997-01-14  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 13  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-935-727-13

Query Match 75.8%; Score 47; DB 9; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.4;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

## RESULT 12

US-09-877-336-2  
Sequence 2, Application US/09877336  
Publication No. US20030000851A1  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung  
TITLE OF INVENTION: METHODS OF USING HUMAN RECEPTOR ON  
TITLE OF INVENTION: PROTEIN 4-1BB  
FILE REFERENCE: 740.011US3  
CURRENT APPLICATION NUMBER: US/09/877,336  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: 09/007,097  
PRIOR FILING DATE: 1998-01-14  
PRIOR APPLICATION NUMBER: 08/409,851  
PRIOR FILING DATE: 1995-03-23  
PRIOR APPLICATION NUMBER: 08/122,796  
PRIOR FILING DATE: 1993-09-16  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-877-336-2

Query Match 75.8%; Score 47; DB 10; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.4;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

## RESULT 13

US-10-097-330-9  
Sequence 9, Application US/10097330

Publication No. US20020127651A1  
GENERAL INFORMATION:  
APPLICANT: Ni et al.  
TITLE OF INVENTION: HUMAN 4-1BB RECEPTOR SPLICING VARIANT  
FILE REFERENCE: PF254D1C2  
CURRENT APPLICATION NUMBER: US/10/097,330  
CURRENT FILING DATE: 2002-03-15  
PRIOR APPLICATION NUMBER: US 09/739,394  
PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: US 09/253,549  
PRIOR FILING DATE: 1999-02-22  
PRIOR APPLICATION NUMBER: US 08/816,605  
PRIOR FILING DATE: 1997-03-13  
PRIOR APPLICATION NUMBER: US 60/013,474  
PRIOR FILING DATE: 1996-03-15  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-097-330-9

Query Match 75.8%; Score 47; DB 13; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.4;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

RESULT 14  
US-10-027-199-2  
Sequence 2, Application US/10027199  
Publication No. US20020168719A1  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung  
TITLE OF INVENTION: NEW RECEPTOR AND RELATED PRODUCTS AND  
METHODS  
FILE REFERENCE: 740.013US2  
CURRENT APPLICATION NUMBER: US/10/027,199  
CURRENT FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/955,572  
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-22  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/461,652  
PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/122,796  
PRIOR FILING DATE: EARLIER FILING DATE: 1993-09-03  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-027-199-2

Query Match 75.8%; Score 47; DB 13; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.4;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

RESULT 15  
US-10-170-997-2  
Sequence 2, Application US/10170997  
Publication No. US20030082157A1  
GENERAL INFORMATION:  
APPLICANT: Kwon, Byoung Se  
TITLE OF INVENTION: New Receptor and Related Products and

Methods  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Barnard, Brown & Michaels  
STREET: 306 East State Street, Suite 220  
CITY: Ithaca  
STATE: NY  
COUNTRY: USA  
ZIP: 14850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/170,997  
FILING DATE: 12-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/955,573  
FILING DATE: 22-OCT-1997  
APPLICATION NUMBER: 08/460,976  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/122,796  
FILING DATE: 13-SEP-1993  
APPLICATION NUMBER: US 08/012,269  
FILING DATE: 01-FEB-1993  
APPLICATION NUMBER: US 07/922,996  
FILING DATE: 30-JUL-1992  
APPLICATION NUMBER: US 08/267,577  
FILING DATE: 07-NOV-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Michaels, Christopher A  
REGISTRATION NUMBER: 34,390  
REFERENCE/DOCKET NUMBER: KWO4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 607-273-1711  
TELEFAX: 607-273-2609  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-170-997-2

Query Match 75.8%; Score 47; DB 14; Length 255;  
Best Local Similarity 72.7%; Pred. No. 3.4;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|||||:  
Db 106 CKQGQELTKKG 116

RESULT 16  
US-10-186-643-11  
Sequence 11, Application US/10186643  
Publication No. US20030118546A1  
GENERAL INFORMATION:  
APPLICANT: Wei, Ying-Fei  
APPLICANT: Ni, Jian  
APPLICANT: Gentz, Reiner  
APPLICANT: Ruben, Steven  
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
FILE REFERENCE: 1488.1280004  
CURRENT APPLICATION NUMBER: US/10/186,643  
CURRENT FILING DATE: 2002-07-02  
PRIOR APPLICATION NUMBER: US/09/573,986  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 11
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-643-11

Query Match      75.8%; Score 47; DB 14; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 17
US-10-207-655-160
; Sequence 160, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 160
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-160

Query Match      75.8%; Score 47; DB 14; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 18
US-10-418-242-13
; Sequence 13, Application US/10418242
; Publication No. US20040013664A1
; GENERAL INFORMATION:
; APPLICANT: Gentz et al.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P3
; CURRENT APPLICATION NUMBER: US/10/418,242
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,604
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/935,727
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,279
; PRIOR FILING DATE: 1999-04-27

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 13
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-418-242-13

Query Match      75.8%; Score 47; DB 15; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTKQG 11
Db      106 CKQGQELTKKG 116

RESULT 19
US-09-898-570-12
; Sequence 12, Application US/09898570
; Patent No. US20020123612A1
; GENERAL INFORMATION:
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 15966-776CIP
; CURRENT APPLICATION NUMBER: US/09/898,570
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/198,293
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/198,645
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/210,809
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/199,476
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,025
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/224,610
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,024
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/199,880
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/218,591
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/271,814
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/215,855
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 09/839,446
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 845
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: POLYX
; OTHER INFORMATION: Z97832_B.0.707
US-09-898-570-12

Query Match      69.4%; Score 43; DB 9; Length 845;
Best Local Similarity 88.9%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CRPGQELTK 9
Db      55 CRPGFELTK 63
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## RESULT 20

US-09-839-446-12  
; Sequence 12, Application US/09839446  
; Publication No. US20030050232A1  
; GENERAL INFORMATION:  
; APPLICANT: GERLACH, VALERIE L.  
; APPLICANT: ELLERMAN, KAREN  
; APPLICANT: MACDOUGALL, JOHN R.  
; APPLICANT: SMITHSON, GLENNDA  
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND  
; TITLE OF INVENTION: METHODS OF USING THE SAME  
; FILE REFERENCE: 15966-776  
; CURRENT APPLICATION NUMBER: US/09/839,446  
; CURRENT FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: 60/198,293  
; PRIOR FILING DATE: 2000-04-19  
; PRIOR APPLICATION NUMBER: 60/198,645  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 60/210,809  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/199,476  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 60/200,025  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 60/224,610  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/200,024  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 60/199,880  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 60/218,591  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 60/271,814  
; PRIOR FILING DATE: 2001-02-27  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 845  
; TYPE: PRT  
; ORGANISM: Unknown.Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: POLYX  
; OTHER INFORMATION: Z97832\_B.0.707  
US-09-839-446-12

Query Match 69.4%; Score 43; DB 10; Length 845;  
Best Local Similarity 88.9%; Pred. No. 62;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
Db 55 CRPGFELTK 63

## RESULT 21

US-10-104-047-2834  
; Sequence 2834, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2834  
; LENGTH: 880  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-104-047-2834

Query Match 69.4%; Score 43; DB 15; Length 880;  
Best Local Similarity 88.9%; Pred. No. 65;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
Db 55 CRPGFELTK 63

## RESULT 22

US-10-239-663-35  
; Sequence 35, Application US/10239663  
; Publication No. US20030139572A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Rizvi, Safia, K.  
; APPLICANT: Smith, Randall, F.  
; APPLICANT: Xiang, Zhaoying  
; APPLICANT: Kabnick, Karen  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50018  
; CURRENT APPLICATION NUMBER: US/10/239,663  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: PCT/US01/09226  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/192,158  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,668  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: 60/200,166  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; LENGTH: 897  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-663-35

Query Match 69.4%; Score 43; DB 14; Length 897;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
Db 184 CRPGFELTK 192

## RESULT 23

US-10-406-073-6  
; Sequence 6, Application US/10406073  
; Publication No. US20030219813A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Ruey-Bing  
; APPLICANT: NG, Chi Kin Domingos  
; APPLICANT: TOMLINSON, James E.  
; APPLICANT: KOMIVES, Laszlo G.  
; APPLICANT: TOPPER, James N.  
; APPLICANT: ROBISON, Keith E.  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED  
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM  
; FILE REFERENCE: MPI02-048PIRNM  
; CURRENT APPLICATION NUMBER: US/10/406,073  
; CURRENT FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: 60/369876  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1

TYPE: PRT

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; FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-073-6

```

```

Query Match      69.4%; Score 43; DB 15; Length 914;
Best Local Similarity 88.9%; Pred. No. 67;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 CRPGQELTK 9
      |||||
Db      184 CRPGFELTK 192

```

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RESULT 24
US-09-898-570-14
; Sequence 14, Application US/09898570
; Patent No. US20020123612A1
; GENERAL INFORMATION:
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 15966-776CIP
; CURRENT APPLICATION NUMBER: US/09/898,570
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/198,293
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/198,645
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/210,809
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/199,476
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,025
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/224,610
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,024
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,591
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/215,855
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 09/839,446
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: POLYX
; OTHER INFORMATION: Z97832_B_1
US-09-898-570-14

```

```

Query Match      69.4%; Score 43; DB 9; Length 974;
Best Local Similarity 88.9%; Pred. No. 72;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 CRPGQELTK 9
      |||||
Db      184 CRPGFELTK 192

```

```

RESULT 25
US-09-839-446-14
; Sequence 14, Application US/09839446
; Publication No. US20030050232A1
; GENERAL INFORMATION:
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 15966-776
; CURRENT APPLICATION NUMBER: US/09/839,446
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 60/198,293
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/198,645
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/210,809
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/199,476
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,025
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/224,610
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,024
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/199,880
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/218,591
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/271,814
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: POLYX
; OTHER INFORMATION: Z97832_B_1
US-09-839-446-14

```

```

Query Match      69.4%; Score 43; DB 10; Length 974;
Best Local Similarity 88.9%; Pred. No. 72;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 CRPGQELTK 9
      |||||
Db      184 CRPGFELTK 192

```

```

RESULT 26
US-10-239-663-36
; Sequence 36, Application US/10239663
; Publication No. US20030139572A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/10/239,663
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158

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; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,668  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: 60/200,166  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 993  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-663-36

Query Match 69.4%; Score 43; DB 14; Length 993;  
Best Local Similarity 88.9%; Pred. No. 73;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELTK 9  
||| |||  
Db 184 CRPGFELTK 192

RESULT 27  
US-10-406-073-8  
; Sequence 8, Application US/10406073  
; Publication No. US20030219813A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Ruey-Bing  
; APPLICANT: NG, Chi Kin Domingos  
; APPLICANT: TOMLINSON, James E.  
; APPLICANT: KOMUVES, Laszlo G.  
; APPLICANT: TOPPER, James N.  
; APPLICANT: ROBISON, Keith E.  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED  
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM  
; FILE REFERENCE: MPI02-048P1RNM  
; CURRENT APPLICATION NUMBER: US/10/406,073  
; CURRENT FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: 60/369876  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; FastSEQ for Windows, Version 4.0  
; SEQ ID NO 8  
; LENGTH: 993  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-406-073-8

Query Match 69.4%; Score 43; DB 15; Length 993;  
Best Local Similarity 88.9%; Pred. No. 73;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELTK 9  
||| |||  
Db 184 CRPGFELTK 192

RESULT 28  
US-10-406-073-15  
; Sequence 15, Application US/10406073  
; Publication No. US20030219813A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Ruey-Bing  
; APPLICANT: NG, Chi Kin Domingos  
; APPLICANT: TOMLINSON, James E.  
; APPLICANT: KOMUVES, Laszlo G.  
; APPLICANT: TOPPER, James N.  
; APPLICANT: ROBISON, Keith E.  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED  
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM

; FILE REFERENCE: MPI02-048P1RNM  
; CURRENT APPLICATION NUMBER: US/10/406,073  
; CURRENT FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: 60/369876  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; FastSEQ for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 993  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-406-073-15

Query Match 69.4%; Score 43; DB 15; Length 993;  
Best Local Similarity 88.9%; Pred. No. 73;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRPGQELTK 9  
||| |||  
Db 184 CRPGFELTK 192

RESULT 29  
US-09-930-512-18  
; Sequence 18, Application US/09930512  
; Publication No. US20040010118A1  
; GENERAL INFORMATION:  
; APPLICANT: Zerhusen, Bryan D  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Spaderna, Steven  
; APPLICANT: Gangolli, Esha A  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Vernet, Corine  
; APPLICANT: Szekeres, Edward S  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Gerlach, Valerie L  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Peyman, John  
; APPLICANT: Stone, David  
; APPLICANT: MacDougall, John  
; TITLE OF INVENTION: No. US20040010118A1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-091  
; CURRENT APPLICATION NUMBER: US/09/930,512  
; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 60/225,692  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: 60/225,837  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: 60/225,693  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: 60/226,236  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/226,353  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 60/227,085  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/227,395  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: 60/227,492  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 60/227,600  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 60/275,952  
; PRIOR FILING DATE: 2001-03-14

; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 1006  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-930-512-18

Query Match 69.4%; Score 43; DB 11; Length 1006;  
Best Local Similarity 88.9%; Pred. No. 74;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
|||||  
Db 219 CRPGFELTK 227

## RESULT 30

US-09-898-570-16  
; Sequence 16, Application US/09898570  
; Patent No. US20020123612A1

## GENERAL INFORMATION:

; APPLICANT: GERLACH, VALERIE L.  
; APPLICANT: ELLERMAN, KAREN  
; APPLICANT: MACDOUGALL, JOHN R.  
; APPLICANT: SMITHSON, GLENDA

; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND  
; TITLE OF INVENTION: METHODS OF USING THE SAME

; FILE REFERENCE: 15966-776CIP

; CURRENT APPLICATION NUMBER: US/09/898,570

; CURRENT FILING DATE: 2001-07-03

; PRIOR APPLICATION NUMBER: 60/198,293

; PRIOR FILING DATE: 2000-04-19

; PRIOR APPLICATION NUMBER: 60/198,645

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: 60/210,809

; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: 60/199,476

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/200,025

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/224,610

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/200,024

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/199,880

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/218,591

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 60/271,814

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 60/215,855

; PRIOR FILING DATE: 2000-07-03

; PRIOR APPLICATION NUMBER: 09/839,446

; PRIOR FILING DATE: 2001-04-19

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 1009

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: POLYX

; OTHER INFORMATION: CG55096-04

US-09-898-570-16

Query Match 69.4%; Score 43; DB 9; Length 1009;  
Best Local Similarity 88.9%; Pred. No. 75;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
|||||  
Db 184 CRPGFELTK 192

## RESULT 31

US-09-839-446-16  
; Sequence 16, Application US/09839446  
; Publication No. US20030050232A1

## GENERAL INFORMATION:

; APPLICANT: GERLACH, VALERIE L.

; APPLICANT: ELLERMAN, KAREN

; APPLICANT: MACDOUGALL, JOHN R.

; APPLICANT: SMITHSON, GLENDA

; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND  
; TITLE OF INVENTION: METHODS OF USING THE SAME

; FILE REFERENCE: 15966-776

; CURRENT APPLICATION NUMBER: US/09/839,446

; CURRENT FILING DATE: 2001-04-19

; PRIOR APPLICATION NUMBER: 60/198,293

; PRIOR FILING DATE: 2000-04-19

; PRIOR APPLICATION NUMBER: 60/198,645

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: 60/210,809

; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: 60/199,476

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/200,025

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/224,610

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/200,024

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/199,880

; PRIOR FILING DATE: 2000-04-26

; PRIOR APPLICATION NUMBER: 60/218,591

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 60/271,814

; PRIOR FILING DATE: 2001-02-27

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 1009

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: POLYX

; OTHER INFORMATION: CG55096-04

US-09-839-446-16

Query Match 69.4%; Score 43; DB 10; Length 1009;  
Best Local Similarity 88.9%; Pred. No. 75;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9

|||||

Db 184 CRPGFELTK 192

## RESULT 32

US-10-220-033-38

; Sequence 38, Application US/10220033

; Publication No. US20030186906A1

## GENERAL INFORMATION:

; APPLICANT: Schlengersiepen, Karl-Hermann

; APPLICANT: Schlengersiepen, Reimar

; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene  
; TITLE OF INVENTION: and a molecule binding to an expression product of that

; FILE REFERENCE: P68119US0

; CURRENT APPLICATION NUMBER: US/10/220,033

; CURRENT FILING DATE: 2003-03-17

; PRIOR APPLICATION NUMBER: PCT/EP01/02694

; PRIOR FILING DATE: 2001-03-10

; PRIOR APPLICATION NUMBER: EP00105190.3

; PRIOR FILING DATE: 2000-03-11

; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
; OTHER INFORMATION: obtained by screening randomly synthesized  
; OTHER INFORMATION: peptides  
US-10-220-033-38

Query Match 66.1%; Score 41; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPQQLTKQG 11  
Db 5 RQQLTKKG 14

## RESULT 33

US-09-746-359A-70  
; Sequence 70, Application US/09746359A  
; Patent No. US20020042366A1  
; GENERAL INFORMATION:

; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Eagan, Maribeth A.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Chandrasekher, Yasmin A.  
; APPLICANT: No. US20020042366A1ak, Julia E.  
; TITLE OF INVENTION: Method for Treating Inflammation  
; FILE REFERENCE: 99-108  
; CURRENT APPLICATION NUMBER: US/09/746,359A  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 70  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-746-359A-70

Query Match 66.1%; Score 41; DB 9; Length 135;  
Best Local Similarity 70.0%; Pred. No. 20;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPQQLTKQG 11  
Db 52 RQQLTKKG 61

## RESULT 34

US-10-424-658-70  
; Sequence 70, Application US/10424658  
; Publication No. US20040005320A1  
; GENERAL INFORMATION:

; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Chandrasekher, Yasmin A.  
; TITLE OF INVENTION: Method for Treating Inflammation

; FILE REFERENCE: 99-108D1  
; CURRENT APPLICATION NUMBER: US/10/424,658  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 09/746,359  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 70  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-424-658-70

Query Match 66.1%; Score 41; DB 15; Length 135;  
Best Local Similarity 70.0%; Pred. No. 20;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPQQLTKQG 11  
Db 52 RQQLTKKG 61

## RESULT 35

US-09-746-359A-67  
; Sequence 67, Application US/09746359A  
; Patent No. US20020042366A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Eagan, Maribeth A.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Chandrasekher, Yasmin A.  
; APPLICANT: No. US20020042366A1ak, Julia E.  
; TITLE OF INVENTION: Method for Treating Inflammation  
; FILE REFERENCE: 99-108  
; CURRENT APPLICATION NUMBER: US/09/746,359A  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 67  
; LENGTH: 196  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-746-359A-67

Query Match 66.1%; Score 41; DB 9; Length 196;  
Best Local Similarity 70.0%; Pred. No. 30;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPQQLTKQG 11  
Db 106 RQQLTKKG 115

## RESULT 36

US-10-424-658-67  
; Sequence 67, Application US/10424658  
; Publication No. US20040005320A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Penny

```
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Blumberg, Hal
; APPLICANT: Chandrasekher, Yasmin A.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108D1
; CURRENT APPLICATION NUMBER: US/10/424,658
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/ 746,359
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-424-658-67
```

```
Query Match 66.1%; Score 41; DB 15; Length 196;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 0;
```

```
QY 2 RPQELTKQG 11
Db 106 RFGMEITKDG 115
```

## RESULT 37

```
US-09-746-359A-59
; Sequence 59, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. US20020042366A1ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-59
```

```
Query Match 66.1%; Score 41; DB 9; Length 201;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 0;
```

```
QY 2 RPQELTKQG 11
Db 111 RFGMEITKDG 120
```

## RESULT 38

```
US-09-912-672A-16
; Sequence 16, Application US/09912672A
; Patent No. US20020164689A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: CLASS II CYTOKINE RECEPTOR-LIKE PROTEINS
; TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 07334-184001
; CURRENT APPLICATION NUMBER: US/09/912,672A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/475,541
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-672A-16
```

```
Query Match 66.1%; Score 41; DB 9; Length 201;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 0;
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```
QY 2 RPQELTKQG 11
Db 111 RFGMEITKDG 120
```

## RESULT 39

```
US-09-925-055D-35
; Sequence 35, Application US/09925055D
; Publication No. US20030157096A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Topouzis, Stavros
; TITLE OF INVENTION: SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-56
; CURRENT APPLICATION NUMBER: US/09/925,055D
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/223,827
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 60/250,876
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-055D-35
```

```
Query Match 66.1%; Score 41; DB 10; Length 201;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 0;
```

```
QY 2 RPQELTKQG 11
Db 111 RFGMEITKDG 120
```

## RESULT 40

```
US-10-424-658-59
; Sequence 59, Application US/10424658
; Publication No. US20040005320A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Blumberg, Hal
; APPLICANT: Chandrasekher, Yasmin A.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108D1
```

```

; CURRENT APPLICATION NUMBER: US/10/424,658
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/ 746,359
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-424-658-59

Query Match      66.1%; Score 41; DB 15; Length 201;
Best Local Similarity 70.0%; Pred.No. 31;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2  RPGQELTKQG 11
Db      111 RPGMEITKDG 120
```

Search completed: May 5, 2004, 14:53:53  
Job time : 4.06849 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:34:41 ; Search time 1.31849 Seconds  
(without alignments)  
802.512 Million cell updates/sec

Title: US-10-067-122B-2\_COPY\_105\_115  
Perfect score: 62  
Sequence: 1 CRPGQELTKQG 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	62	100.0	256	2	B32393	T-cell antigen 4-1
2	47	75.8	255	2	I38426	Lymphocyte activat
3	39	62.9	684	2	T30652	probable RNA helic
4	38	61.3	413	1	VHVN1H	nucleoprotein - in
5	38	61.3	417	2	T34561	hypothetical prote
6	38	61.3	713	1	UMMS	period clock prote
7	38	61.3	1334	2	E86451	probable copia-typ
8	37	59.7	110	2	S52156	protamine - fruit
9	37	59.7	110	2	S52158	protamine - fruit
10	37	59.7	203	2	I49054	Ly-49G.2 antigen -
11	37	59.7	515	2	S54592	hypothetical prote
12	37	59.7	1102	2	T17367	potassium channel
13	37	59.7	1372	2	T25933	hypothetical prote
14	37	59.7	2871	2	A55624	fibrillin-1 precur
15	36	58.1	202	2	AB2148	30S ribosomal prot
16	36	58.1	404	1	VHVNHS	nucleoprotein - he
17	36	58.1	404	1	JQ1531	nucleoprotein - he
18	36	58.1	404	2	S34562	nucleocapsid prote
19	36	58.1	995	2	A56599	embryo kinase 5 -
20	36	58.1	1620	2	T27283	hypothetical prote
21	36	58.1	1894	2	JC4980	plexin 1 precursor
22	36	58.1	2550	2	B53435	vesicular transpor
23	35	56.5	85	2	S52155	male germ-line spe
24	35	56.5	110	2	S52157	protamine - fruit
25	35	56.5	117	2	AE0740	probable exported
26	35	56.5	129	2	S06075	unci protein - Vib
27	35	56.5	240	2	T49856	probable Alp11 hom
28	35	56.5	285	1	C70873	probable enoyl-CoA
29	35	56.5	303	2	AH2016	hypothetical prote

ALIGNMENTS

RESULT 1

B32393  
T-cell antigen 4-1BB precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 21-Jul-2000  
C;Accession: B32393; I48879  
R;Kwon, B.S.; Weissman, S.M.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
A;Title: cDNA sequence of two inducible T-cell genes.  
A;Reference number: A32393; MUID:89184547; PMID:2784565  
A;Accession: B32393  
A;Molecule type: mRNA  
A;Residues: 1-256 <KWO>  
A;Cross-references: GB:J04492; NID:G201121; PIDN:AAA40167.1; PID:G201122  
R;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994  
A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.  
A;Reference number: I48879; MUID:94179805; PMID:8133039  
A;Accession: I48879  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-256 <RES>  
A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178

C;Genetics:  
A;Intons: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: transmembrane protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 100.0%; Score 62; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.00085;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
Db 105 CRPGQELTKQG 115

RESULT 2

I38426  
Lymphocyte activation-induced receptor ILA precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000  
C;Accession: I38426; JT0752  
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R  
Eur. J. Immunol. 24, 2219-2227, 1994  
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.  
A;Reference number: I38426; MUID:94374434; PMID:8088337  
A;Accession: I38426  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA



R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E86451

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1334 <STO>

A;Cross-references: GB:AE005172; NID:g10092575; PIDN:AAG12968.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

C;Superfamily: retrovirus-related polyprotein

Query Match 61.3%; Score 38; DB 2; Length 1334;  
Best Local Similarity 77.8%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PGQELTKQG 11

|||||:|

Db 1096 PGQKLTKAG 1104

RESULT 8

S52156

protamine - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 07-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 24-Sep-1998

C;Accession: S52156

R;Russell, S.R.

submitted to the EMBL Data Library, November 1994

A;Description: Drosophila melanogaster mst35B genes encode very similar protamine like m

A;Reference number: S52155

A;Accession: S52156

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-110 <RUS>

A;Cross-references: EMBL:246784; NID:g608697; PID:g608698

C;Genetics:

A;Gene: FlyBase:Mst35Bb

A;Cross-references: FlyBase:FBgn0013301

Query Match 59.7%; Score 37; DB 2; Length 110;  
Best Local Similarity 54.5%; Pred. No. 17;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

|||||:|

Db 69 CAPSQKCSKQG 79

RESULT 9

S52158

protamine - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 07-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 24-Sep-1998

C;Accession: S52158

R;Russell, S.R.

submitted to the EMBL Data Library, November 1994

A;Description: Drosophila melanogaster mst35B genes encode very similar protamine like m

A;Reference number: S52155

A;Accession: S52158

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-110 <RUS>

A;Cross-references: EMBL:246785; NID:g608701; PID:g608702

C;Genetics:

A;Gene: FlyBase:Mst35Bb

A;Cross-references: FlyBase:FBgn0013301

Query Match 59.7%; Score 37; DB 2; Length 110;  
Best Local Similarity 54.5%; Pred. No. 17;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11

|||||:|

Db 69 CAPSQKCSKQG 79

RESULT 10

I49054

Ly-49G.2 antigen - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 17-Mar-2000

C;Accession: I49054

R;Smith, H.R.; Karhofer, F.M.; Yokoyama, W.M.

J. Immunol. 153, 1068-1079, 1994

A;Title: Ly-49 multigene family expressed by IL-2-activated NK cells.

A;Reference number: I49049; MUID:94300068; PMID:8027540

A;Accession: I49054

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-203 <RES>

A;Cross-references: EMBL:U10095; NID:g533497; PIDN:AAA50223.1; PID:g533498

C;Superfamily: natural killer cell receptor P1; C-type lectin homology

Query Match 59.7%; Score 37; DB 2; Length 203;  
Best Local Similarity 66.7%; Pred. No. 30;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9

|||||:|

Db 109 CRPGNDLLK 117

RESULT 11

S54592

hypothetical protein YMR285c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YMR285c

C;Species: Saccharomyces cerevisiae

C;Date: 08-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 19-Apr-2002

C;Accession: S54592; A42461

R;Pearson, D.; Bowman, S.

submitted to the EMBL Data Library, May 1995

A;Reference number: S54582

A;Accession: S54592

A;Molecule type: DNA

A;Residues: 1-515 <PEA>

A;Cross-references: EMBL:249704; NID:g825540; PID:g825551; MIPS:YMR285c

A;Experimental source: strain AB972

R;Kang, W.; Matsushita, Y.; Grohmann, L.; Graack, H.R.; Kitakawa, M.; Isono, K.

J. Bacteriol. 173, 4013-4020, 1991

A;Title: Cloning and analysis of the nuclear gene for Yml33, a protein of the large subur

A;Reference number: A42461; MUID:91286184; PMID:2061283

A;Accession: A42461

A;Molecule type: DNA

A;Residues: 1-68, 'A', 70-86, 'W', 88, 'ARAA', 93, 'YQKT', 98-105, 'Q' <KAN>

A;Cross-references: GB:D90217

C;Genetics:

A;Gene: SGD:NGL2

A;Cross-references: SGD:S0004898

A;Map position: 13R

C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC936.11c

Query Match 59.7%; Score 37; DB 2; Length 515;  
Best Local Similarity 47.1%; Pred. No. 68;  
Matches 8; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 1 CR-----PGQELTKQG 11

|||||:|

Db 477 CRGFLRMPGPNEMTKHG 493

# RESULT 12

Tl7367  
potassium channel protein elkl - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: Tl7367  
R;Shi, W.; Wang, H.S.; Pan, Z.; Wymore, R.; Cohen, I.S.; McKinnon, D.; Dixon, J.E.  
J. Physiol. 511, 675-682, 1998  
A;Title: Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution in  
A;Reference number: Z18731; MUID:98382545; PMID:9714851  
A;Accession: Tl7367  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1102 <SHI>  
A;Cross-references: EMBL:AF061957; NID:g3659689; PID:g3659690; PIDN:AAC61520.1  
C;Genetics:  
A;Gene: elkl  
C;Function:  
A;Description: may play a role in the sympathetic nervous system  
C;Keywords: potassium channel

Query Match 59.7%; Score 37; DB 2; Length 1102;  
Best Local Similarity 54.5%; Pred. No. 1.3e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|:|:|:|:  
Db 572 CAPGEYLLRQG 582

# RESULT 13

T25933  
hypothetical protein W02C12.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T25933  
R;Murray, J.; Wohldmann, P.  
submitted to the EMBL Data Library, December 1996  
A;Description: The sequence of C. elegans cosmid W02C12.  
A;Reference number: Z20112  
A;Accession: T25933  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1372 <MUR>  
A;Cross-references: EMBL:U80815; PIDN:AAB37995.1; GSPDB:GN00022; CESP:W02C12.1  
A;Experimental source: strain Bristol N2; clone W02C12  
C;Genetics:  
A;Gene: CESP:W02C12.1  
A;Map position: 4  
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1

Query Match 59.7%; Score 37; DB 2; Length 1372;  
Best Local Similarity 60.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 10  
|:|:|:|:|:  
Db 1098 CKPGQFLVKE 1107

# RESULT 14

A55624  
fibrillin-1 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 24-Nov-2003  
C;Accession: A55624  
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995  
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene  
A;Reference number: A55624; MUID:95130561; PMID:7829516

A;Accession: A55624  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2871 <YIN>  
A;Cross-references: GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510  
C;Genetics:  
A;Gene: Fbn-1  
C;Superfamily: fibrillin; EGF homology  
F;1201-1236/Domain: EGF homology <EGF>

Query Match 59.7%; Score 37; DB 2; Length 2871;  
Best Local Similarity 54.5%; Pred. No. 3.1e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
|:|:|:|:|:  
Db 1835 CKPGYRLTSTG 1845

# RESULT 15

AB2148  
30S ribosomal protein S4 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C;Accession: AB2148  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AB2148  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-202 <KUR>  
A;Cross-references: GB:BA000019; PIDN:BA074436.1; PID:g17131830; GSPDB:GN00179  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: rps4  
C;Superfamily: Escherichia coli ribosomal protein S4

Query Match 58.1%; Score 36; DB 2; Length 202;  
Best Local Similarity 71.4%; Pred. No. 45;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQEL 7  
|:|:|:|:  
Db 131 CRPGEEI 137

# RESULT 16

VHVNHS  
nucleoprotein - hemorrhagic septicemia virus  
N;Alternate names: nucleocapsid protein  
C;Species: hemorrhagic septicemia virus  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Jun-2000  
C;Accession: A36651  
R;Bernard, J.; Lecocq-Xhonneux, F.; Rossius, M.; Thiry, M.E.; de Kinkelin, P.  
J. Gen. Virol. 71, 1669-1674, 1990  
A;Title: Cloning and sequencing the messenger RNA of the N gene of viral haemorrhagic septicemia virus  
A;Reference number: A36651; MUID:90362052; PMID:2202782  
A;Accession: A36651  
A;Molecule type: mRNA  
A;Residues: 1-404 <BER>  
A;Cross-references: GB:D00687; NID:g222771; PIDN:BAA00591.1; PID:g222772  
C;Genetics:  
A;Gene: N  
C;Superfamily: infectious hematopoietic necrosis virus nucleoprotein  
C;Keywords: nucleocapsid; nucleoprotein

Query Match 58.1%; Score 36; DB 1; Length 404;  
Best Local Similarity 75.0%; Pred. No. 84;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
QY      2  RPQQLTK 9
      ||||:|
Db      184  RPQQLTK 191

RESULT 17
JQ1531
nucleoprotein - hemorrhagic septicemia virus (strain Makah)
N;Alternate names: nucleocapsid protein
C;Species: hemorrhagic septicemia virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: JQ1531; S21836
R;Bernard, J.; Bremont, M.; Winton, J.
J. Gen. Virol. 73, 1011-1014, 1992
A;Title: Nucleocapsid gene sequence of a North American isolate of viral haemorrhagic septicemia virus
A;Reference number: JQ1531; MUID:92341050; PMID:1634868
A;Accession: JQ1531
A;Molecule type: mRNA
A;Residues: 1-404 <BER>
A;Cross-references: EMBL:X59241; NID:G60410; PIDN:CAA41930.1; PID:G60411
C;Genetics:
A;Gene: N
C;Superfamily: infectious hematopoietic necrosis virus nucleoprotein
C;Keywords: nucleocapsid; nucleoprotein

Query Match      58.1%; Score 36; DB 1; Length 404;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2  RPQQLTK 9
      ||||:|
Db      184  RPQQLTK 191

RESULT 18
S34562
nucleocapsid protein - hemorrhagic septicemia virus
C;Species: hemorrhagic septicemia virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C;Accession: S34562
R;Schuetze, H.
Submitted to the EMBL Data Library, June 1993
A;Reference number: S34562
A;Accession: S34562
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <SCH>
A;Cross-references: EMBL:X73873; NID:G395126; PIDN:CAA52077.1; PID:G395127
C;Genetics:
A;Gene: n
C;Superfamily: infectious hematopoietic necrosis virus nucleoprotein
C;Keywords: nucleocapsid

Query Match      58.1%; Score 36; DB 2; Length 404;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2  RPQQLTK 9
      ||||:|
Db      184  RPQQLTK 191

RESULT 19
A56599
embryo kinase 5 - chicken
N;Alternate names: receptor tyrosine kinase Csk5
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Gallus gallus (chicken)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 04-Feb-2000
C;Accession: A56599
R;Pasquale, E.B.
Cell Regul. 2, 523-534, 1991

A;Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor-
A;Reference number: A56599; MUID:92144672; PMID:1664238
A;Accession: A56599
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-995 <PAS>
A;Cross-references: GB:M62325; NID:G211448; PIDN:AAA48667.1; PID:G211449
A;Note: sequence extracted from NCBI backbone (NCBIN:81999, NCBIIP:82001)
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat hc
C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kin
F;628-896/Domain: protein kinase homology <KIN>
F;636-644/Region: protein kinase ATP-binding motif
F;919-985/Domain: SAM homology <SAM>

Query Match      58.1%; Score 36; DB 2; Length 995;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1  CRPQQLTKQ 11
      ||||:|
Db      264  CRPGYSEVNG 274

RESULT 20
T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27283
R;Ainscough, R.
Submitted to the EMBL Data Library, September 1999
A;Reference number: T20336
A;Accession: T27283
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1620 <WIL>
A;Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f
A;Experimental source: clone Y64G10A
C;Genetics:
A;Gene: CESP:Y64G10A.f
A;Introns: 77/1, 116/1, 198/1, 282/1, 365/1, 425/1, 466/1, 548/1, 559/1, 601/1, 625/1, 711/1

Query Match      58.1%; Score 36; DB 2; Length 1620;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1  CRPQQLTKQ 11
      ||||:|
Db      492  CERPGESENG 502

RESULT 21
JC4980
plexin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 05-Nov-1999
C;Accession: JC4980
R;Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa,
Biochem. Biophys. Res. Commun. 226, 524-529, 1996
A;Title: Identification of a neuronal cell surface molecule, plexin, in mice.
A;Reference number: JC4980; MUID:96400291; PMID:8806667
A;Accession: JC4980
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1894 <KAM>
A;Cross-references: DDBJ:D86948; NID:G1665756; PIDN:BAA13188.1; PID:d1013877; PID:G16657
A;Experimental source: brain
C;Comment: This protein is a membrane protein, and plays a role in neuronal cell contact
sence of calcium ions.
C;Keywords: duplication; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;513-561,659-704,807-859/Region: cysteine-rich
F;1238-1264/Domain: transmembrane #status predicted <TM>
```

F:1266-1268/Region: hydrophilic

Query Match 58.1%; Score 36; DB 2; Length 1894;  
 Best Local Similarity 77.8%; Pred. No. 3.3e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CRPGQELTKQ 10  
 |||||  
 Db 317 RFGQALAKQ 325

RESULT 22

B53435  
 vesicular transport-associated repeat protein Tb-292 - Trypanosoma brucei  
 N;Alternate names: membrane-associated protein Tb-292  
 C;Species: Trypanosoma brucei  
 C;Date: 26-May-1995 #sequence\_revision 07-Jul-1995 #text\_change 07-May-1999  
 C;Accession: B53435; S34395  
 R;Lee, M.G.S.; Russell, D.G.; D'Alessandro, P.A.; Van der Ploeg, L.H.T.  
 J. Biol. Chem. 269, 8408-8415, 1994  
 A;Title: Identification of membrane-associated proteins in Trypanosoma brucei encoding a  
 A;Reference number: A53435; MUID:94179225; PMID:8132566  
 A;Accession: B53435  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-189,558-721,'P',723-738,'D',740-829,'L',831-1100,'Q',1102-1636,'L',1638-16  
 418,'H',2420-2499,'L',2501-2550 <LE2>  
 A;Cross-references: EMBL:X73956  
 R;Lee, M.; Russell, D.; D'Alessandro, P.; van der Ploeg, L.  
 submitted to the EMBL Data Library, December 1992  
 A;Description: Identification of membrane associated proteins in Trypanosoma brucei enco  
 A;Reference number: S34394  
 A;Accession: S34395

A;Molecule type: mRNA  
 A;Residues: 1-2550 <LE2>  
 A;Cross-references: EMBL:X73956; NID:g3933395; PID:g3933396  
 C;Keywords: tandem repeat  
 F:74-557/Region: 8-residue repeats (A-R-L-R-A-E-E-E)  
 Query Match 58.1%; Score 36; DB 2; Length 2550;  
 Best Local Similarity 63.6%; Pred. No. 4.3e+02;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11  
 |||||  
 Db 1470 CRPHSENTDQ 1480

RESULT 23

S52155  
 male germ-line specific protamine - fruit fly (Drosophila melanogaster)  
 C;Species: Drosophila melanogaster  
 C;Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 24-Sep-1998  
 C;Accession: S52155  
 R;Russell, S.R.

submitted to the EMBL Data Library, November 1994  
 A;Description: Drosophila melanogaster mst35B genes encode very similar protamine like m  
 A;Reference number: S52155  
 A;Accession: S52155  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-85 <RUS>  
 A;Cross-references: EMBL:Z46790; NID:g608695; PID:g608696  
 C;Genetics:  
 A;Gene: FlyBase:Mst35Ba  
 A;Cross-references: FlyBase:FBgn0013300

Query Match 56.5%; Score 35; DB 2; Length 85;  
 Best Local Similarity 54.5%; Pred. No. 32;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11  
 |||||

Db 44 CAPRQCKSKQG 54

RESULT 24

S52157  
 protamine - fruit fly (Drosophila melanogaster)  
 C;Species: Drosophila melanogaster  
 C;Date: 07-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 24-Sep-1998  
 C;Accession: S52157  
 R;Russell, S.R.

submitted to the EMBL Data Library, November 1994  
 A;Description: Drosophila melanogaster mst35B genes encode very similar protamine like m  
 A;Reference number: S52155  
 A;Accession: S52157  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-110 <RUS>  
 A;Cross-references: EMBL:Z46783; NID:g608699; PID:g608700  
 C;Genetics:  
 A;Gene: FlyBase:Mst35Ba  
 A;Cross-references: FlyBase:FBgn0013300

Query Match 56.5%; Score 35; DB 2; Length 110;  
 Best Local Similarity 54.5%; Pred. No. 40;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQ 11  
 |||||  
 Db 69 CAPRQCKSKQG 79

RESULT 25

AE0740  
 probable exported protein STY2079 [imported] - Salmonella enterica subsp. enterica serov  
 C;Species: Salmonella enterica subsp. enterica serovar Typhi  
 A;Note: this species has also been called Salmonella typhi  
 C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C;Accession: AE0740  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
 th, T.; Conner, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
 A;Reference number: AB0502; MUID:21534947; PMID:11677608  
 A;Accession: AE0740  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-117 <PAR>  
 A;Cross-references: GB:AL513382; PIDN:CAD05624.1; PID:g16503121; GSPDB:GN00176  
 C;Genetics:  
 A;Gene: STY2079  
 C;Superfamily: Escherichia coli hypothetical protein b1839

Query Match 56.5%; Score 35; DB 2; Length 117;  
 Best Local Similarity 85.7%; Pred. No. 43;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQEL 7  
 |||||  
 Db 47 CRPGQAL 53

RESULT 26

S06075  
 unci protein - Vibrio alginolyticus  
 C;Species: Vibrio alginolyticus  
 C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Oct-1999  
 C;Accession: S06075  
 R;Krumholz, L.R.; Esser, U.; Simoni, R.D.  
 Nucleic Acids Res. 17, 7993-7994, 1989  
 A;Title: Nucleotide sequence of the unc operon of Vibrio alginolyticus.  
 A;Reference number: S06075; MUID:90016889; PMID:2529481

A;Accession: S06075  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-129 <KRU>  
A;Cross-references: EMBL:X16050; NID:G48331; PIDN:CAA34174.1; PID:G48332  
C;Genetics:  
A;Gene: uncI  
C;Superfamily: uncI protein

Query Match 56.5%; Score 35; DB 2; Length 129;  
Best Local Similarity 66.7%; Pred. No. 46;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RPQQLTKQ 10  
|||:|:  
Db 7 RPQRELARQ 15  
|||:|:

RESULT 27  
T49856  
probable Alp11 homolog of tubulin-folding cofactor B [imported] - Neurospora crassa  
N;Alternate names: protein B24P11.120  
C;Species: Neurospora crassa  
C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C;Accession: T49856  
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000  
A;Reference number: 225022  
A;Accession: T49856  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-240 <SCH>  
A;Cross-references: EMBL:AL356833; GSPDB:GN00116; NCSP:B24P11.120  
A;Experimental source: BAC clone B24P11; strain OR74A  
C;Genetics:  
A;Gene: NCSP:B24P11.120  
A;Map position: 6  
A;Introns: 79/3

Query Match 56.5%; Score 35; DB 2; Length 240;  
Best Local Similarity 54.5%; Pred. No. 81;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRPQQLTKQ 11  
|||:|:  
Db 156 CRVQDDTRRG 166  
|||:|:

RESULT 28  
C70873  
probable enoyl-CoA hydratase - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C;Accession: C70873  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: C70873  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-285 <COL>  
A;Cross-references: GB:AL021184; GB:AL123456; NID:G3261498; PIDN:CAA16000.1; PID:G279140  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: echA12  
C;Superfamily: naphthoate synthase; enoyl-CoA hydratase homology  
F;41-201/Domain: enoyl-CoA hydratase homology <ECH>

Query Match 56.5%; Score 35; DB 1; Length 285;

Best Local Similarity 77.8%; Pred. No. 94;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RPQQLTKQ 10  
|||:|:  
Db 226 RPQIELTKR 234  
|||:|:

RESULT 29  
AH2016  
hypothetical protein all1686 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 24-Nov-2003  
C;Accession: AH2016  
R;Xaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S. DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AH2016  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-303 <KUR>  
A;Cross-references: GB:BA000019; PIDN:BA078052.1; PID:G17135506; GSPDB:GN00179  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all1686  
C;Superfamily: tartrate-resistant acid phosphatase

Query Match 56.5%; Score 35; DB 2; Length 303;  
Best Local Similarity 70.0%; Pred. No. 99;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RPQQLTKQ 11  
|||:|:  
Db 104 RPQDLTKQ 113  
|||:|:

RESULT 30  
T14058  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Neolamprologus brichardi mitochondrion  
C;Species: mitochondrion Neolamprologus brichardi  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
C;Accession: T14058  
R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F. Mol. Phylogenet. Evol. 4, 420-432, 1995  
A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.  
A;Reference number: Z17790; MUID:96360498; PMID:8747298  
A;Accession: T14058  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-348 <KOC>  
A;Cross-references: EMBL:U07255; NID:G463956; PID:G463957; PIDN:AAC59804.1  
A;Experimental source: strain T47a; isolate PSU  
C;Genetics:  
A;Genome: mitochondrion  
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2  
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

Query Match 56.5%; Score 35; DB 2; Length 348;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QELTKQ 11  
|||:|:  
Db 267 QELTKQ 273  
|||:|:

RESULT 31  
T14034  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Julidochromis marlieri mitochondrion  
C;Species: mitochondrion Julidochromis marlieri

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
 C;Accession: T14034  
 R;Koehler, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.  
 Mol. Phylogenet. Evol. 4, 420-432, 1995  
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.  
 A;Reference number: Z17790; MUID:96360498; PMID:8747298  
 A;Accession: T14034  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-348 <KOC>  
 A;Cross-references: EMBL:U07249; NID:G463944; PID:G463945; PIDN:AAC59798.1  
 A;Experimental source: strain T1a; PSU  
 C;Genetics:  
 A;Genome: mitochondrion  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2  
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11  
 |||||  
 Db 267 QELTKQG 273

RESULT 32  
 T14206  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Tanganicodus irsacae mitochondri  
 C;Species: mitochondrion Tanganicodus irsacae  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
 C;Accession: T14206  
 R;Koehler, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.  
 Mol. Phylogenet. Evol. 4, 420-432, 1995  
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.  
 A;Reference number: Z17790; MUID:96360498; PMID:8747298  
 A;Accession: T14206  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-348 <KOC>  
 A;Cross-references: EMBL:U07265; NID:G463976; PID:G463977; PIDN:AAC59814.1  
 A;Experimental source: strain T13a; PSU  
 C;Genetics:  
 A;Genome: mitochondrion  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2  
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11  
 |||||  
 Db 267 QELTKQG 273

RESULT 33  
 T14118  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Nile tilapia mitochondrion  
 C;Species: mitochondrion Tilapia nilotica, Oreochromis niloticus (Nile tilapia)  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
 C;Accession: T14118  
 R;Koehler, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.  
 Mol. Phylogenet. Evol. 4, 420-432, 1995  
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.  
 A;Reference number: Z17790; MUID:96360498; PMID:8747298  
 A;Accession: T14118  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-348 <KOC>  
 A;Cross-references: EMBL:U07258; NID:G463962; PID:G463963; PIDN:AAC59806.1  
 A;Experimental source: strain T77a; isolate PSU  
 C;Genetics:

A;Genome: mitochondrion  
 A;Genetic code: SGC1  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2  
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11  
 |||||  
 Db 267 QELTKQG 273

RESULT 34  
 T14140  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Perissodus microlepis mitochondri  
 C;Species: mitochondrion Perissodus microlepis  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
 C;Accession: T14140  
 R;Koehler, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.  
 Mol. Phylogenet. Evol. 4, 420-432, 1995  
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.  
 A;Reference number: Z17790; MUID:96360498; PMID:8747298  
 A;Accession: T14140  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-348 <KOC>  
 A;Cross-references: EMBL:U07260; NID:G463966; PID:G463967; PIDN:AAC59809.1  
 A;Experimental source: strain T32a; PSU  
 C;Genetics:  
 A;Genome: mitochondrion  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2  
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11  
 |||||  
 Db 267 QELTKQG 273

RESULT 35  
 T14128  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Paracryprichromis brieni mitochondri  
 C;Species: mitochondrion Paracryprichromis brieni  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
 C;Accession: T14128  
 R;Koehler, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.  
 Mol. Phylogenet. Evol. 4, 420-432, 1995  
 A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.  
 A;Reference number: Z17790; MUID:96360498; PMID:8747298  
 A;Accession: T14128  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-348 <KOC>  
 A;Cross-references: EMBL:U07259; NID:G463964; PID:G463965; PIDN:AAC59808.1  
 A;Experimental source: strain T40a; isolate PSU  
 C;Genetics:  
 A;Genome: mitochondrion  
 A;Genetic code: SGC1  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2  
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11  
 |||||  
 Db 267 QELTKQG 273

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-348 <KOC>

A;Cross-references: EMBL:U07266; NID:g463978; PID:g463979; PIDN:AAC59817.1

A;Experimental source: strain T49a; PSU

C;Genetics:

A;Genome: mitochondrion

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11

|||||

Db 267 QELTKQG 273

RESULT 39

T14216

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Xenotilapia flavipinnus mitochondrion

C;Species: mitochondrion Xenotilapia flavipinnus

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002

C;Accession: T14216

R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.

Mol. Phylogenet. Evol. 4, 420-432, 1995

A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.

A;Reference number: Z17790; MUID:96360498; PMID:8747298

A;Accession: T14216

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-348 <KOC>

A;Cross-references: EMBL:U07269; NID:g463984; PID:g463985; PIDN:AAC59818.1

A;Experimental source: strain T12a; PSU

C;Genetics:

A;Genome: mitochondrion

A;Superfamily: NADH dehydrogenase (ubiquinone) chain 2

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11

|||||

Db 267 QELTKQG 273

RESULT 40

T14200

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Pseudotropheus sp. mitochondrion

C;Species: mitochondrion Pseudotropheus sp.

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002

C;Accession: T14200

R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.

Mol. Phylogenet. Evol. 4, 420-432, 1995

A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.

A;Reference number: Z17790; MUID:96360498; PMID:8747298

A;Accession: T14200

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-348 <KOC>

A;Cross-references: EMBL:U07263; NID:g463972; PID:g463973; PIDN:AAC59812.1

C;Genetics:

A;Genome: mitochondrion

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11

|||||

Db 267 QELTKQG 273

RESULT 36

T13839

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Buccochromis lepturus mitochondrion

C;Species: mitochondrion Buccochromis lepturus

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002

C;Accession: T13839

R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.

Mol. Phylogenet. Evol. 4, 420-432, 1995

A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.

A;Reference number: Z17790; MUID:96360498; PMID:8747298

A;Accession: T13839

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-348 <KOC>

A;Cross-references: EMBL:U07241; NID:g463928; PID:g463929; PIDN:AAC59788.1

A;Experimental source: strain JAC 2

C;Genetics:

A;Genome: mitochondrion

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11

|||||

Db 267 QELTKQG 273

RESULT 37

T14122

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Ophthalmotilapia ventralis mitochondrion

C;Species: mitochondrion Ophthalmotilapia ventralis

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002

C;Accession: T14122

R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.

Mol. Phylogenet. Evol. 4, 420-432, 1995

A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.

A;Reference number: Z17790; MUID:96360498; PMID:8747298

A;Accession: T14122

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-348 <KOC>

A;Cross-references: EMBL:U07257; NID:g463960; PID:g463961; PIDN:AAC59807.1

A;Experimental source: strain T10a; isolate PSU

C;Genetics:

A;Genome: mitochondrion

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 56.5%; Score 35; DB 2; Length 348;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QELTKQG 11

|||||

Db 267 QELTKQG 273

RESULT 38

T14209

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Telmatochromis temporalis mitochondrion

C;Species: mitochondrion Telmatochromis temporalis

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002

C;Accession: T14209

R;Kocher, T.D.; Conroy, J.A.; McKaye, K.R.; Stauffer, J.R.; Lockwood, S.F.

Mol. Phylogenet. Evol. 4, 420-432, 1995

A;Title: Evolution of NADH dehydrogenase subunit 2 in East African cichlid fish.

A;Reference number: Z17790; MUID:96360498; PMID:8747298

A;Accession: T14209

Qy 5 QELTKOG 11  
| | | | |  
Db 267 QELTKOG 273

Search completed: May 5, 2004, 14:41:21  
Job time : 1.31849 secs

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:30:56 ; Search time 0.866438 Seconds

(without alignments)

661.065 Million cell updates/sec

Title: US-10-067-122B-2\_COPY\_105\_115

Perfect score: 62

Sequence: 1 CRPGQELTKQG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	62	100.0	256	1 TNR9_MOUSE	P20334 mus musculus
2	47	75.8	255	1 TNR9_HUMAN	Q07011 homo sapien
3	42	67.7	639	1 BMP9_STRPU	P98069 strongyloce
4	40	64.5	297	1 XEDA_HUMAN	Q9hav5 homo sapien
5	39	62.9	228	1 TR18_MOUSE	Q35714 mus musculus
6	39	62.9	684	1 NTP2_MCV1	Q98218 molluscum c
7	38	61.3	413	1 NCAP_IHNV	P19691 infectious
8	38	61.3	672	1 PHX5_MOUSE	P08399 mus musculus
9	37	59.7	416	1 TR19_MOUSE	Q9j113 mus musculus
10	37	59.7	423	1 TR19_HUMAN	Q9ns68 homo sapien
11	37	59.7	514	1 EDAR_ORYLA	Q90vy2 oryzias lat
12	37	59.7	515	1 YMSO_YEAS	Q03264 saccharomyc
13	37	59.7	876	1 KCH8_MOUSE	P59111 mus musculus
14	37	59.7	986	1 Z445_MOUSE	Q8r2v3 mus musculus
15	37	59.7	1031	1 Z445_HUMAN	P59923 homo sapien
16	37	59.7	1102	1 KCH8_RAT	Q9gws8 rattus norv
17	37	59.7	1107	1 KCH8_HUMAN	Q96142 homo sapien
18	37	59.7	2871	1 FBN1_MOUSE	Q61554 mus musculus
19	36.5	58.9	372	1 PEXC_ARATH	Q9m841 arabidopsis
20	36	58.1	202	1 RS4_ANASP	Q8yti0 anabaena sp
21	36	58.1	404	1 NCAP_VHSV0	P24378 viral hemor
22	36	58.1	404	1 NCAP_VHSVM	P27371 viral hemor
23	36	58.1	1004	1 EPB2_CHICK	P28693 gallus gall
24	36	58.1	1075	1 MTR3_MOUSE	Q8k296 mus musculus
25	36	58.1	1198	1 MTR3_HUMAN	Q13615 homo sapien
26	35	56.5	129	1 ATP2_VIBAL	P12983 vibrio algi
27	35	56.5	285	1 ECHC_MYCTU	O53163 mycobacteri
28	35	56.5	349	1 NU2M_ONCMY	P48175 oncorhynchu
29	35	56.5	349	1 NU2M_SALSA	Q35924 salmo salar
30	35	56.5	385	1 ARGD_THEMEA	Q9x2a5 thermotoga
31	35	56.5	705	1 CIR_HUMAN	P00736 homo sapien
32	35	56.5	887	1 MCM2_DROME	P49735 drosophila
33	35	56.5	1342	1 RPOB_BUCAP	P41184 buchnera ap

#### RESULT 1

TNR9\_MOUSE

ID TNR9\_MOUSE STANDARD; PRT; 256 AA.

AC P20334;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).

GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89184547; PubMed=2784565;

RA Kwon B.S., Weissman S.M.;

RT "cDNA sequences of two inducible T-cell genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RX MEDLINE=94179805; PubMed=8133039;

RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;

RT "Genomic Organization and chromosomal localization of the T-cell antigen 4-1BB.";

RL J. Immunol. 152:2256-2262(1994).

RN [3]

RP CHARACTERIZATION, AND SEQUENCE OF 25-29.

RX MEDLINE=93139510; PubMed=7678621;

RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,

RT "Inducible T cell antigen 4-1BB. Analysis of expression and function.";

RL J. Immunol. 150:771-781(1993).

CC -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.

CC -!- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER. ASSOCIATES WITH P56-LCK. Interacts with TRAF1, TRAF2 AND TRAF3 (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.

CC -!- INDUCTION: Optimal by PMA and ionomycin.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

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CC EMBL; J04492; AAA40167.1; -.

CC EMBL; U02567; AAA93113.1; -.

DR PIR; B32393; B32393.  
 DR PDB; 1D0J; 26-SEP-01.  
 DR MGI; MGI:1101059; Tnfrsf9.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 1.  
 DR SMART; SM00208; TNFR; 2.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE NEG.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; 3D-structure.  
 FT SIGNAL 1 24  
 FT CHAIN 25 256  
 FT DOMAIN 25 187  
 FT TRANSMEM 188 208  
 FT DOMAIN 209 256  
 FT REPEAT 17 45  
 FT REPEAT 46 85  
 FT REPEAT 86 117  
 FT REPEAT 118 159  
 FT DISULFID 28 37  
 FT DISULFID 31 44  
 FT DISULFID 47 61  
 FT DISULFID 64 77  
 FT DISULFID 67 85  
 FT DISULFID 87 93  
 FT DISULFID 98 105  
 FT DISULFID 101 116  
 FT DISULFID 119 133  
 FT DISULFID 139 158  
 FT CARBOHYD 128 128  
 FT CARBOHYD 138 138  
 SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 100.0%; Score 62; DB 1; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 0.00023;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
 DB 105 CRPGQELTKQG 115

RESULT 2  
 TNFR9 HUMAN STANDARD; PRT; 255 AA.  
 ID TNFR9 HUMAN  
 AC Q07011;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)  
 DE (CD137 antigen).  
 GN TNFRSF9 OR ILA OR CD137.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=94374434; PubMed=8088337;  
 RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,  
 RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;  
 RA "Molecular and biological characterization of human 4-1BB and its  
 RT ligand.";  
 RL Eur. J. Immunol. 24:2219-2227(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=94085794; PubMed=8262389;  
 RA Schwarz H., Tuckwell J., Lotz M.;  
 RA "A receptor..."

RT family";  
 RL Gene 134:295-298(1993).  
 RN [3]  
 RP REVISION TO 107.  
 RA Schwarz H.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=95347766; PubMed=7622190;  
 RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,  
 RA Kwon B.S.;  
 RT "Characterization of human homologue of 4-1BB and its ligand.";  
 RL Immunol. Lett. 45:67-73(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Pearce A.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer M.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP INTERACTION WITH TRAF1; TRAF2 AND TRAF3.  
 RX MEDLINE=98078711; PubMed=9418902;  
 RA Arch R.H., Thompson C.B.;  
 RT "4-1BB and Ox40 are members of a tumor necrosis factor (TNF)-nerve  
 RT growth factor receptor subfamily that bind TNF receptor-associated  
 RT factors and activate nuclear factor kappaB.";  
 RL Mol. Cell. Biol. 18:558-565(1998).  
 RN [8]  
 RP INTERACTION WITH TRAF1 AND TRAF2.  
 RX MEDLINE=98270914; PubMed=9607925;  
 RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,  
 RA Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,  
 RA Watts T.H.;  
 RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by  
 RT 4-1BB ligand.";  
 RL J. Exp. Med. 187:1849-1862(1998).  
 RN [9]  
 RP INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.  
 RX MEDLINE=21662677; PubMed=11804328;  
 RA Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;  
 RT "A novel leucine-rich repeat protein (LRR-1): potential involvement in  
 RT 4-1BB-mediated signal transduction.";  
 RL Mol. Cells 12:304-312(2001).  
 CC -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T  
 CC cell activation.  
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2 AND TRAF3. Interacts with  
 CC LRR-repeat protein 1/LRR-1.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein



Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKQG 11  
 |||||:|  
 Db 559 CRPGYELSSDG 569

RESULT 4  
 XEDA HUMAN STANDARD; PRT; 297 AA.  
 AC Q9HAV5;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member XEDAR (X-linked  
 ectodysplasin-A2 receptor) (EDA-A2 receptor).  
 GN XEDAR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF GLU-256.  
 RC TISSUE=Fetal kidney;  
 RX MEDLINE=20495245; PubMed=11039935;  
 RA Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,  
 de Vos A.M., Gao W.-Q., Dixit V.M.;  
 RT "Two-amino acid molecular switch in an epithelial morphogen that  
 regulates binding to two distinct receptors.";  
 RL Science 290:523-527(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.J., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Receptor for EDA isoform A2, but not for EDA isoform  
 A1. Mediates the activation of NF-kappa-B. Activation seems to  
 be mediated by binding to TRAF6.  
 CC -!- SUBUNIT: Associates with TRAF1, TRAF3 and TRAF6.  
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein.  
 CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 -----  
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 -----  
 CC EMBL; AF298812; AAG28761.1; -  
 CC EMBL; BC034919; AAH34919.1; -  
 CC MIM; 300276; -  
 CC GO; GO:0005031; F:tumor necrosis factor receptor activity; NAS.

DR GO; GO:0008544; P:epidermal differentiation; NAS.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SMC0208; TNFR; 2.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00505; TNFR\_NGFR\_2; 2.  
 KW Receptor; Developmental protein; Differentiation; Transmembrane;  
 KW Glycoprotein; Repeat.  
 FT DOMAIN 1 138  
 FT TRANSMEM 139 159  
 FT  
 FT DOMAIN 160 297  
 FT REPEAT 2 41  
 FT REPEAT 43 83  
 FT REPEAT 85 118  
 FT DISULFID 3 15  
 FT DISULFID 18 31  
 FT DISULFID 21 41  
 FT DISULFID 44 58  
 FT DISULFID 61 75  
 FT DISULFID 64 83  
 FT DISULFID 86 104  
 FT DISULFID 107 118  
 FT CARBOHYD 74 74  
 FT MUTAGEN 256 256  
 FT SEQUENCE 297 AA; 32728 MW; 0E71127C6C48240C CRC64;  
 SQ

Query Match 64.5%; Score 40; DB 1; Length 297;

Best Local Similarity 77.8%; Pred. No. 4.1;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9

|||||:

Db 21 CGPGQELSK 29

## RESULT 5

## TR18 MOUSE

ID TR18 MOUSE STANDARD; PRT; 228 AA.

AC Q35714; Q9JKR1; Q9JKR2; Q9JKR3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 18 precursor

(Glucocorticoid-induced TNFR-related protein).

GN TNFRSF18 OR GITR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

[1]

RP SEQUENCE FROM N.A. (ISOFORM A).

RC STRAIN=C3H;

RX MEDLINE=97322352; PubMed=9177197;

RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,

Moraca R., Migliorati G., Riccardi C.;

RT "A new member of the tumor necrosis factor/nerve growth factor

receptor family inhibits T cell receptor-induced apoptosis.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).

[2]

RP SEQUENCE FROM N.A. (ISOFORM A).

RC STRAIN=BA1B/C;

RX MEDLINE=20256302; PubMed=10798444;

RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,

Delfino D., Migliorati G., Riccardi C.;

RT "Gene structure and chromosomal assignment of mouse GITR, a member of

the tumor necrosis factor/nerve growth factor receptor family.";

RL DNA Cell Biol. 19:205-217(2000).

[3]

RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).

RC TISSUE=Thymus;

RX MEDLINE=20292073; PubMed=10836847;

RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,

RA Brunetti L., Migliorati G., Riccardi C.;  
RT "Identification of three novel mRNA splice variants of GTR.";  
RL Cell Death Differ. 7:408-410(2000).  
CC -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in  
CC interactions between activated T lymphocytes and endothelial cells  
CC and in the regulation of T cell receptor-mediated cell death.  
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway (By  
CC similarity).  
CC -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and  
CC TRAF6 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms A, B and  
CC C); secreted (isoform D).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=A;  
CC IsoId=O35714-1; Sequence=Displayed;  
CC Name=B;  
CC IsoId=O35714-2; Sequence=VSP\_006510;  
CC Name=C;  
CC IsoId=O35714-3; Sequence=VSP\_006511;  
CC Name=D;  
CC IsoId=O35714-4; Sequence=VSP\_006509;  
CC -!- TISSUE SPECIFICITY: Preferentially expressed in activated T  
CC lymphocytes.  
CC -!- INDUCTION: Upregulated in peripheral mononuclear cells after  
CC antigen stimulation/lymphocyte activation.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -----  
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CC -----  
DR EMBL; U82534; AAB81243.1; -;  
DR EMBL; AF109216; AAF14231.1; -;  
DR EMBL; AF229432; AAF61566.1; -;  
DR EMBL; AF229433; AAF61567.1; -;  
DR EMBL; AF229434; AAF61568.1; -;  
DR MGD; MGI:894675; Tnfrsf18.  
DR InterPro; IPR006210; IEFG.  
DR InterPro; IPR001368; TNFR\_c6.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE\_NEG.  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
KW Alternative splicing.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 228 TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER 18.  
FT DOMAIN 20 153 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 154 174 POTENTIAL.  
FT DOMAIN 175 228 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 28 61 TNFR-CYS 1.  
FT REPEAT 62 101 TNFR-CYS 2.  
FT REPEAT 102 142 TNFR-CYS 3.  
FT DISULFID 29 44 BY SIMILARITY.  
FT DISULFID 62 74 BY SIMILARITY.  
FT DISULFID 69 82 BY SIMILARITY.  
FT DISULFID 103 122 BY SIMILARITY.  
FT DISULFID 116 141 BY SIMILARITY.  
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 121 228 NCSQGLTMTFPGNKTNNVAVCIPEPLTEQYGHLLTVIFLVM  
FT AACIFLLTVQLGLHIWQLRRQHMCPRETQPEAEVQLSAED  
FT ACSFPPEEREGTEKCHLGRWP -> KPAIRGGAVV  
FT S (in isoform D).  
FT /FTId=VSP\_006509.

FT VARSPLIC 189 228 ETQPFQAEVQLSAEDACSFQFPPEEREGTEKCHLGRWP  
FT -> VLIQRPESHRRSCQLRLMLAASSLRNAGSRQKSVI  
FT WGVGGHEAWSSVPPQARYKTCFPAIPLVRAGAMLCIDPWAW  
FT PCSPQQRKWKVYESGELRLGPMMAFLI (in isoform  
FT B).  
FT /FTId=VSP\_006510.  
FT ETQPFQAEVQLSAEDACSFQFPPEEREGTEKCHLGRWP  
FT -> GQLCPREGENVSQAPHLPPQFYRDPAIRGGAVVS (in  
FT isoform C).  
FT /FTId=VSP\_006511.  
SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;  
Query Match 62.9%; Score 39; DB 1; Length 228;  
Best Local Similarity 54.5%; Pred.No. 4.8;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CRPGQELTKQ 11  
Db 82 CQPGQRVESQ 92  
RESULT 6  
NTP2\_MCV1 STANDARD; PRT; 684 AA.  
ID NTP2\_MCV1  
AC Q98218;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Nucleoside triphosphatase II (EC 3.6.1.15) (NTPase II) (Nucleoside  
DE triphosphate phosphohydrolase II) (NPH II).  
GN 50R.  
OS Molluscum contagiosum virus subtype 1 (MCV1).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Molluscipoxvirus.  
OX NCBI\_TaxID=10280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96325459; PubMed=8670425;  
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,  
RA Moss B.;  
RT "Genome sequence of a human tumorigenic poxvirus: prediction of  
RT specific host response-evasion genes.";  
RL Science 273:813-816(1996).  
CC -!- FUNCTION: ESSENTIAL FOR VIRAL REPLICATION. PLAYS AN IMPORTANT ROLE  
CC DURING TRANSCRIPTION OF EARLY MRNAs, PRESUMABLY BY PREVENTING R-  
CC LOOP FORMATION BEHIND THE ELONGATING RNA POLYMERASE. ACTS AS NTP-  
CC DEPENDENT HELICASE THAT CATALYZES UNIDIRECTIONAL UNWINDING OF  
CC 3'-TAILED DUPLEX RNAs. MIGHT ALSO PLAY A ROLE IN THE EXPORT OF  
CC NEWLY SYNTHESIZED MRNA CHAINS OUT OF THE CORE INTO THE CYTOPLASM.  
CC REQUIRED FOR PROPAGATION OF VIRAL PARTICLES (BY SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: NTP + H(2)O = NDP + phosphate.  
CC -!- SIMILARITY: Belongs to the DEAD box helicase family. DEAH  
CC subfamily.  
CC -----  
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CC -----  
DR EMBL; U60315; AAC55178.1; -;  
DR PIR; T30652; T30652.  
DR InterPro; IPR001410; DEAD.  
DR InterPro; IPR002464; DEAH\_box.  
DR InterPro; IPR001650; Helicase\_C.  
DR Pfam; PF00271; Helicase\_C; 1.  
DR SMART; SM00487; DEXDC; 1.  
DR SMART; SM00490; HELICC; 1.  
DR PROSITE; PS00690; DEAH\_ATP\_HELICASE; 1.  
KW ATP-binding; Helicase; Hydrolase; Transcription.  
FT DOMAIN 305 520 HELICASE.

FT NP BIND 197 204 ATP (BY SIMILARITY).  
FT SITE 308 311 DEXH BOX.  
SQ SEQUENCE 684 AA; 76556 MW; 51072BL93CCC7284 CRC64;

Query Match 62.9%; Score 39; DB 1; Length 684;  
Best Local Similarity 63.6%; Pred. No. 16;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRPGQELTKG 11  
|||||:  
Db 117 CRPGLELREAG 127

## RESULT 7

NCAP\_IHNV STANDARD; PRT; 413 AA.  
AC P19691;

DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-MAY-1992 (Rel. 22, Last annotation update)  
DE Nucleocapsid protein (Nucleoprotein).  
GN N.  
OS Infectious hematopoietic necrosis virus (strain Round Butte) (IHNV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Rhabdoviridae; Novirhabdovirus.  
OX NCBI\_TaxID=11291;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89073771; PubMed=3201758;  
RA Gilmore R.D. Jr., Leong J.C.;  
RT "The nucleocapsid gene of infectious hematopoietic necrosis virus, a  
fish rhabdovirus.";  
RL Virology 167:644-648(1988).  
CC -!- PTM: Phosphorylated.  
CC -!- SIMILARITY: TO VHSV NUCLEOCAPSID PROTEIN.

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CC -----  
DR EMBL; J04321; AAA46240.1; -.  
DR PIR; A31834; VHVNIH.  
DR InterPro; IPR004902; Rhabdo\_ncap\_2.  
DR Pfam; PF03216; Rhabdo\_ncap\_2; 1.  
KW Nucleocapsid; Phosphorylation.  
SQ SEQUENCE 413 AA; 45700 MW; 5E2AFF659BBEE38 CRC64;

Query Match 61.3%; Score 38; DB 1; Length 413;  
Best Local Similarity 87.5%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPQQLTK 9  
|||||:  
Db 183 RPQQLTK 190

## RESULT 8

PHX5\_MOUSE STANDARD; PRT; 672 AA.  
AC P08399;

DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Per-hexamer repeat protein 5.  
GN PHX5 OR PER.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

RN SEQUENCE FROM N.A.  
RX MEDLINE=86014384; PubMed=2413365;  
RA Shin H.S., Bargiello T.A., Clark B.T., Jackson F.R., Young M.W.;  
RT "An unusual coding sequence from a Drosophila clock gene is conserved  
RT in vertebrates.";  
RL Nature 317:445-448(1985).  
CC -!- SIMILARITY: TO OTHER G-T STRETCH CONTAINING PROTEINS.

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CC -----  
DR EMBL; M12039; AAA88320.1; -.  
DR EMBL; X02966; CAA26710.2; -.  
DR PIR; A24403; UMMS.  
DR MGD; MGI:104521; Phxr5.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR006210; IEGF.  
DR SMART; SM00181; EGF; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
KW Repeat.  
FT DOMAIN 59 672 G-T REPEATS.  
SQ SEQUENCE 672 AA; 57924 MW; E85BF428CF424C0B CRC64;

Query Match 61.3%; Score 38; DB 1; Length 672;  
Best Local Similarity 77.8%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRPGQELTK 9  
|||||:  
Db 23 CRPGFELAK 31

## RESULT 9

TR19\_MOUSE STANDARD; PRT; 416 AA.  
ID TR19\_MOUSE STANDARD; PRT; 416 AA.  
AC Q9JLL3; Q9JHF1; Q9JH6; Q9JLL2; Q9QXW7;

DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 19 precursor  
DE (Toxicity and JNK inducer) (TRADE).  
GN TNFRSF19 OR TROY OR TAJ.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 4).  
RX MEDLINE=20054362; PubMed=10585776;  
RA Hu S., Tamada K., Ni J., Vincenz C., Chen L.;  
RT "Characterization of TNFRSF19, a novel member of tumor necrosis factor  
RT receptor superfamily.";  
RL Genomics 62:103-107(1999).

## [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX TISSUE=Embryo, and Spleen;  
RX MEDLINE=20270246; PubMed=10809768;

RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;  
RT "TAJ, a novel member of the tumor necrosis factor receptor family,  
RT activates the c-Jun N-terminal kinase pathway and mediates  
RT caspase-independent cell death.";  
RL J. Biol. Chem. 275:15336-15342(2000).

## [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).  
RX TISSUE=Brain;  
RX MEDLINE=20347167; PubMed=10764796;

RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
RT "TAJ, a novel member of the tumor necrosis factor receptor family,  
RT activates the c-Jun N-terminal kinase pathway and mediates  
RT caspase-independent cell death.";  
RL J. Biol. Chem. 275:15336-15342(2000).



```

RN RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Can mediate activation of JNK and NF-kappa-B. May
CC promote caspase-independent cell death.
CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3 and TRAF5.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=TAJ-alpha, TRADEalpha;
CC IsoId=Q9NS68-1; Sequence=Displayed;
CC Name=2; Synonyms=TRADEbeta;
CC IsoId=Q9NS68-2; Sequence=VSP_006512;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in prostate. Detected at
CC lower levels in thymus, spleen, testis, uterus, small intestine,
CC colon and peripheral blood leukocytes.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
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CC -----
DR EMBL; AF167555; AAF71828.1; -
DR EMBL; AB040434; BAB03269.1; -
DR EMBL; AF246998; AAK28395.1; -
DR EMBL; AF246999; AAK28396.1; -
DR EMBL; BC047321; AAK47321.1; -
DR Genew; HGNC:11915; TNFRSF19.
DR MIM; 606122; -
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; NAS.
DR GO; GO:0006917; P:induction of apoptosis; NAS.
DR GO; GO:0007254; P:JNK cascade; NAS.
DR InterPro; IPR001368; TNFR_c5.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW Alternative splicing.
FT SIGNAL 1 29
FT CHAIN 30 423
FT DOMAIN 30 170
FT TRANSMEM 171 191
FT DOMAIN 192 423
FT REPEAT 33 72
TNFR-CYS 1.
POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 19.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.

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FT REPEAT 74 114
FT REPEAT 116 149
FT DISULFID 34 46
FT DISULFID 49 62
FT DISULFID 52 72
FT DISULFID 75 89
FT DISULFID 92 106
FT DISULFID 95 114
FT DISULFID 117 135
FT DISULFID 138 149
FT CARBOHYD 105 105
FT VARSPLIC 416 423
TNFR-CYS 2.
TNFR-CYS 3.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
VRQRLGSL -> EA (in isoform 2).
/FTID=VSP_006512.
S -> T (IN REF. 3; AAK28396).
T -> A (IN REF. 1).
GS -> ET (IN REF. 1).
F -> L (IN REF. 3; AAK28396).
T -> A (IN REF. 3; AAK28396).
V -> I (IN REF. 3).
SQ SEQUENCE 423 AA; 46015 MW; B5891CEA9ED45361 CRC64;
Query Match 59.7%; Score 37; DB 1; Length 423;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CRPGQELTKQ 10
Db 52 CGPGMELSKE 61
RESULT 11
EDAR_ORYLA STANDARD; PRT; 514 AA.
ID EDAR_ORYLA STANDARD; PRT; 514 AA.
AC Q90VY2; Q90Z36;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member EDAR precursor
DE (Ectodysplasin-A receptor) (Reduced scale-3 protein).
GN EDAR OR RS-3.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OC NCBI_TaxID=8090;
RN [1]
SEQUENCE FROM N.A.
STRAIN=AA2, and HNI;
MEDLINE=21407746; PubMed=11516953;
Kondo S., Kuwahara Y., Kondo M., Naruse K., Mitani H., Wakamatsu Y.,
Ozato K., Asakawa S., Shimizu N., Shima A.;
"The medaka rs-3 locus required for scale development encodes
ectodysplasin-A receptor."
Curr. Biol. 11:1202-1206(2001).
-!- FUNCTION: Receptor for EDA (By similarity). May mediate the
activation of NF-kappa-B and JNK.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- DEVELOPMENTAL STAGE: Barely detectable on the body surface of 8
and 15 day old fish. In 30 day old fish, when scale development
has started, expression is high in patches of epithelial cell
clusters and at the posterior margins of growing scales.
-!- SIMILARITY: Contains 3 TNFR-Cys repeats.
-!- SIMILARITY: Contains 1 death domain.
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